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55.932 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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908470 seqs, 133250620 residues Gapop 10.0 , Gapext 0.5 1 YRLAIRRIALRY 12 US-08-653-294C-36 58 **BLOSUM62** Scoring table: Perfect score: Sequence: Searched: Title:

Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Minimum DB seq length: 0 Maximum DB seq length: 60

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A\_Geneseq\_101002: Database

Listing first 45 summaries

| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	HLA-B2702 84-79-84	Peptide B2702.84-7	Immunomodulating d	HLA-B2702 84-75-84	HLA-B2702 CTL modu	Immunomodulating d	HLA-B2702 CTL modu	HLA-B2702 CTL modu	Peptide B2702.84-7	Peptide B2702.84-7
ΠD	~	AAW33798	AAW33799	AAR95428	AAR92907	AAW33778	AAR92909	AAR92908	AAW33791	AAW33792
DB	16	19	19	16	16	13	16	16	19	13
% Query e Match Length DB I	12	12	12	20	20	50	20	20	20	20
% Query Match	100.0	100.0	100.0	75.9	75.9	75.9	67.2	67.2	67.2	67.2
Score	28	28	28	44	44	44	39	39	39	39
Result No.	1	7	m	4	'n	v	7	80	6	10

HIA-B2702 84-75T/7 Human MHC 1 alpha Human immune/haema HLA-B2702 CTL modu Immunomodulating d HLA-B2702 CTL modu Peptide B2702.84-7 Curvularia verrucu E.Coli DMAJ 22 imm Human HDJI immunog Peptide #4804 enco Human prostate can Human reproductive Propionibacterium Propionibacterium Propionibacterium Human ORNEX protein Human Restractium Human Restractium Human Restractium Human Restractium Human Restractium	Propionibacterium Backbone cyclised Human interleukin- Peptide #1 used in Peptide #2 used in Immunomodulatory p Immunomodulatory p Immunosuppressive Human Class I HLA- Peptide fragment o Alphal-helix of HL HLA-B2702 CTL modu T-cell modulating T-cell modulating Peptide B2702 CTL modu
16 AAR95430 25 AAM83083 26 AAM83083 26 AAM83083 16 AAR92911 19 AAW33779 16 AAW33793 21 AAU98851 22 AAU2828 22 AAU3828 23 AAU986134 22 AAU3968 23 AAU43856	22 AAUS6052 22 AAB8912 22 AAB8912 19 AAW33781 19 AAW37263 19 AAW47263 19 AAW47263 19 AAW47263 16 AAR59450 16 AAR89450 16 AAR89062 16 AAR80062 16 AAR800512 17 AAW07512 17 AAW07513
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## ALIGNMENTS

HLA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; reall lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell. AAR95429 standard; peptide; 12 AA. HLA-B2702 84-79-84 palindrome. 94WO-US12985 93US-0150493 12-NOV-1996 (first entry) WO9513288-A1. 10-NOV-1994; 10-NOV-1993; 18-MAY-1995. Synthetic. AAR95429; RESULT 1 AAR95429 THE STANDARD STANDARD

(STRD ) UNIV LELAND STANFORD JUNIOR. Clayberger C, Krensky AM; WPI; 1995-194027/25. Compsns. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.

human-leucocyte-associated antigens. This sequence represents the HIA-B2702 84-79-84 palindrome. These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HIA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HIA-B2702.60-84 (see AAR95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate

AAR95413, and AAR95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the

Example;

Page 12; 29pp; English

compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.

Matches Query Match

12;

Conservative

0,

Local

Similarity

100.0%;

Score 58; DB 16; Pred. No. 0.00026; Mismatches 0;

Length 12; Indels

0, Gaps

0,

Sequence

12

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RESULT 2
AAW33798
CXXX PPTX XXXXX
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                 Example 1; Page 19; 41pp; English.
                                            New immunomodulating dimer peptide(s) - based alpha-1 domain, used for preventing rejection
                                                                          WPI; 1998-086530/08
                                                                                                                                   24-MAY-1996;
                                                                                                                                                                         27-NOV-1997
                                                                                                                                                                                           WO9744351-A1.
                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                  transplantation;
                                                                                                                                                                                                                                                                              Peptide B2702.84-79/79-84 tested for immunomodulating activity
                                                                                                                                                                                                                                                                                                 19-JUN-1998
                                                                                                                                                                                                                                                                                                                     AAW33798
                                                                                                                                                                                                                                                                                                                                       AAW33798 standard; peptide; 12
                                                                                                                                                      22-MAY-1997;
                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                          rejection.
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                                                                                                                 (STRD ) UNIV LELAND STANFORD JUNIOR.
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                                      autoimmune diseases
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                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                    96US-0653294
                                                                                                                                                       97WO-US08689
                                                                                                                                                                                                                                                  dimer; immunosuppressant drug; CTL activation;
autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                             Ç
                                                                                              Krensky AM
                                               on a Class I HLA-B
of transplants or
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Peptides AAW33784-98 and AAW33778-9 were assayed for their

This sequence represents a specifically claimed immunomodulating dimer peptide of the invention. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or estexified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or

Claim 17; Page 35; 41pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cc immunomodulating activity. A peptide-type compound or variant is claimed combined which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, cc and/or C-terminal amidated or esterified forms of up to 60 amino acids, cc where the peptide-type compound comprises the formula; A-B, where A, B = CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa84 = a hydrophobic or cc small amino acid; aa82 = R or L; aa83 = G or R; and as represents amino acid. Sequences in the brackets may optionally be absent or truncated cat any peptide type bond within the brackets. The compounds comprise can any acid sequences related to a Class I HLA-B alphal domain (positions CC amino acid sequences related to a Class I HLA-B alphal domain (positions CC undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in creamons are or for treating autoinmune diseases. a c. diabetes.
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                                                                                                                                                                                                                                                                                                                      24-MAY-1996;
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                                                                                                                                                                                                                                                  Beulow R, Clayberger C,
                                                                                                                                                                                                                                                                                                                                                   22 MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transplantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunomodulating dimer peptide
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                                                                                                                                                                                                                                                                                     (STRD ) UNIV LELAND STANFORD JUNIOR.
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autoimmune disease; Class I HLA-B alpha-1 doma
                                                                                                                                                                                                                                                    Krensky AM;
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                                                                                                                                                                 a Class I HLA-B
transplants or
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V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a represents amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid; The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HLA.B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptides or proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
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12 AA; Sequence

Gaps ö Query Match 100.0%; Score 58; DB 19; Length 12; Best Local Similarity 100.0%; Pred. No. 0.00026; Matches 12; Conservative 0; Mismatches 0; Indels

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1 YRLAIRRIALRY 12

AAR95428 standard; peptide; 20 AA. 12-NOV-1996 (first entry) AAR95428 

HLA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell. HLA-B2702 84-75-84 palindrome.

Synthetic

WO9513288-A1

18-MAY-1995

94WO-US12985 10-NOV-1994;

93US-0150493 10-NOV-1993;

Krensky AM;

(STRD ) UNIV LELAND STANFORD JUNIOR.

Clayberger C,

WPI; 1995-194027/25.

AAR95413, and AAR95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the than 82702 84-75-84 palindrome. These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. P74 is found in a limited number of cell types, but is particularly expressed on B and T cells. P74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see AAR95416), induces calcium influx, and inhibits Compsns. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs. Example; Page 12; 29pp; English.

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cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCs), by audding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.
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RESULT 5 AAR92907

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AAR92907 standard; peptide; 20 AA.

AAR92907;

HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).

Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.

Synthetic.

WO9526979-A1

12-0CT-1995.

95WO-US04349 05-APR-1995; 94US-0222851. 05-APR-1994; (STRD ) UNIV LELAND STANFORD JUNIOR.

Clayberger C, Krensky AM, Parham P;

WPI; 1995-358582/46,

Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient 

Example 15; Page 36; 80pp; English.

of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs) AAR83061-R83085, AAR83090-R83096 and AAR92907-R92914 represent fragments

20 AA; Sequence

Gaps . 8 Score 44; DB 16; Length 20; Pred. No. 0.17; 0; Mismatches 0; Indels 75.9%; 12; Conservative Query Match Best Local Similarity Matches 12; Conserv

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RESULT 6
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                                                                                                                                               cc amino acids, where the peptide-type compound comprises the formula; A-B, cwhere A, B = (R aa76-771) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or CC V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84= a cC hydrophobic or small amino acid; aa82 = R or I; aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be CC absent or truncated at any peptide type bond within the brackets. The CC compounds comprise amino acid sequences related to a class I HLA-B CC alphal domain (positions 79-84). They can be used to inhibit cytotoxic C I-lymphocytes (CTL) from undesirably attacking cells in a host or in CC virto. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the CC used for preventing rejection of transplants or for treating autoimune CC diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. CC The products can also be used for detection and diagnosis.
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Best Local (
                                                                Matches
                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                     acylated and/or C-terminal amidated or esterified forms of up to 60
                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a specifically claimed immunomodulating dimer peptide of the invention. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
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transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clayberger C,
                                                                                                                          20
                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                           75.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                             0;
                                                             Score 44; DB
Pred. No. 0.17
0; Mismatches
                                                                             DB 19; Length 20 0.17;
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                                                                Indels
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RESULT 8
AAR922008
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AAR92909
ID AAR9
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; the class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                             AAR92908 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-358582/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR92909;
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                                                                                                                         HLA-B2702 CTL
                                                                                                                                                                                16-MAY-1996
                                                                                                                                                                                                                                             AAR92908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR83061-R83085, AAR83090-R83096 and AAR92907-R92913 represent fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 15; Page 36; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-APR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YRLAIR-----RIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                               YRLAIRLNERRENLRTALRY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry
                                                                                                                   modulating peptide (B2702.84-75(T)/75-84).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modulating peptide (B2702.84-75/75-84(T)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Krensky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0222851.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.2%;
55.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB Pred. No. 1.4; 0; Mismatches
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1.4;
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immunomodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-771) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, Sor N; aa79 = R or G, aa80 = I or N, aa81, a848 = a hydrophobic or amil amino acid; aa82 = R or L; aa83 = G or R; and ar expresents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undestrably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection or fransplants or for treating autoimmune diseases, e.g. diabetes, the cheumatoid arthritis and lupus erythematosis. The products can also be the manner of the companies of transplants or for treating autoimmune diseases, e.g. diabetes, the manner of the companies of the companies or proteins or the products can also be the custom and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                           New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New immunomodulating dimer peptide(s) - based on a Class I HLA-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide B2702.84-75/75-84T tested for immunomodulating activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8;
                                                                                                                                                                                              Peptides AAW33784-98 and AAW33778-9 were assayed for their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 19; Length 20;
Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.2%; Scur.
55.0%; Pred. No. 1...
0; Mismatches
  Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                        Example 1; Page 19; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW33792 standard; peptide; 20 AA.
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Clayberger C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 55.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beulow R, Clayberger C,
                                      WPI; 1998-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAY-1997;
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  Beulow R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW33792;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 of class I major introductions and ANKY2V07-R22914 represent fragments sequence is an inverted diner of residues 75-84 of the alpha-1 domain the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR83061-R83085, AAR83090-R83096 and AAR92907-R92914 represent fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                            Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide B2702.84-75T/75-84 tested for immunomodulating activity.
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8
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                                                                                                                                                                                                                                                 Krensky AM, Parham P;
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                                                                                                                                                                                                          (STRD ) UNIV LELAND STANFORD JUNIOR
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                                                                                                                                 95WO-US04349.
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                                                                                                                                                                                                                                                 Clayberger C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
Homo sapiens.
                                                      WO9526979-A1
                                                                                                                                                                        05-APR-1994;
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                                                                                                                                 05-APR-1995;
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                                                                                           12-OCT-1995
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                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunomodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = CR aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = CD, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and as represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise condesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, red additional activities and lupus erythematosis. The products can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Example; Page 12; 29pp; English
                                                                                                                              WPI; 1995-194027/25.
                                                                                                                                                                             Clayberger C,
                                                                                                                                                                                                                                                                                 10-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                       W09513288-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA; p74; alphal-helix; T-cell lysate; membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating
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                                                                                                                                                                                                                                                                                                                                   10-NOV-1994;
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                                                                                                                                                                                                                               (STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain, used for preventing rejection of transplants or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                               cytolytic
                                               comprising lymphoid surface membrane proteins -cytolytic activity and differentiation of CTLs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection and diagnosis.
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                                                                                                                                                                                Krensky
                                                                                                                                                                                                                                                                                 93US-0150493
                                                                                                                                                                                                                                                                                                                                      94WO-US12985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases
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55.0%;
                                                                                                                                                                                AM;
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Pred. No. 1.4;
0; Mismatches
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                                                                                 which may
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AAR95415-R95431 represent palindromes and

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RESULT 12
AAR71429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Major histocompatibility complex class 1; MHC 1; cell receptor; alpha 1 domain; peptide [Ala81]-Dk-(69-85); interaction modulation; arthritis; neoplasias; lupus erythematosus.
          AAR71424-R71438 are human major histocompatibility complex class 1 (MHC 1) alpha 1 domain derived peptides and peptide mutants, they were used to modulate interactions between MHC 1 and cell surface receptors. Via competitive inhibition the peptides diminish the receptors response, this feature may be useful for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human MHC 1 alpha 1 domain peptide [Ala81]-Dk-(69-85)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                               Example 4; Page 45; 103pp; English
                                                                                                                                                                   Regulating cell surface interaction between MHC
                                                                                                                                                                                                                                                          Goldstein A,
                                                                                                                                                                                                                                                                                                                                                                12-AUG-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                       WPI; 1995-098577/13.
                                                                                                                                                                                                                                                                                                                              12-AUG-1993;
                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA
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                                                                                                                                                                                                                                                           Goodenow
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57.9%;
                                                                                                                                                                                                                                                          RS,
                                                                                                                                                                   receptor response - class I antigen and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                           Olsson
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Pred. No.
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                                                                                                                                                                     by modulating
the cell surface
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2000US-0234223
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20-OCT-2000;
20-OCT-2000;
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20-OCT-2000;
20-OCT-2000;
80-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
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                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                         Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
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                                              Score 35; DB 16; Length 18; Pred. No. 7.1; 2; Indels
                                                                                                                                                                                                                                                                                                            Human immune/haematopoietic antigen SEQ ID NO:10676.
                                                                                                                                                                                                                 AAM83083 standard; Protein; 46 AA.
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2000US-0205615.
2000US-0211486.
2000US-0216647.
2000US-0216680.
2000US-0217486.
2000US-0217486.
2000US-0217487.
2000US-0220964.
2000US-0220964.
2000US-0220964.
2000US-0225218.
2000US-0225218.
2000US-0225218.
2000US-0225218.
2000US-0225218.
2000US-0225218.
2000US-0225218.
                                         Query Match 60.3%;
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JAN-2001; 2001WO-US01354
                                                                                                                                                                                                                                                                            07-NOV-2001 (first entry)
                                                                                                      1 YRLAIRRIALRY 12
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| FRVDLRTLALRY 17
                 18 AA;
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                 Sequence
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AMM 3083

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AAM 83

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RESULT 14
AAR92911
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                                                                                                                                                                                                                                                    CC AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic contrivity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC collynucleotides may be used to produce the secreted (I), by inserting CC polynucleotides may be used to produce the secreted (I), by inserting CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169 CC represent sequences used in the exemplification of the present invention.
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Matches
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01-DEC-2000
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05-DEC-2000
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08-DEC-2000
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17-NOV-2000;
17-NOV-2000;
16-MAY-1996
                          AAR92911;
                                                     AAR92911 standard;
                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
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                                                                                                                                                 1 YRLAIRRIAL 10
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YKLGVRRMAL 18
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                                                                                                                                                                           Similarity 6; Conserv
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                                                                                                                                                                                                                               46
                                                                                                                                                                             Conservative
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2000US-0251990.
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                                                                                                                                                                                                                               AA;
                                                     peptide;
                                                                                                                                                                                        60.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ruben
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Pred. No. 18;
3; Mismatches
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RESULT 15
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                    AAW33779 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                            Synthetic
                                                                                                                  Immunomodulating transplantation;
                                                                                                                                                                                     19-JUN-1998
                                                                                                                                                                                                            AAW33779;
                                                                                                                                                                                                                                                                                                                                                                                                                                   of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 15; Page 36; 80pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-1994;
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                                                                                                       rejection.
                                                                                                                                                        Immunomodulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
                                                              domo sapiens
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                                                                                                                                                                                                                                                                                                                              1 YRLAIR----RIALR 11
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                                                                                                                dimer; immunosuppressant drug; CTL activation;
autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                         dimer peptide
                                                                                                                                                                                                                                                                                                                                                                   59.5%;
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27-NOV-1997 WO9744351-A1.

Query Match 59.5%; Score 34.5; DB 19; Length 20; Best Local Similarity 56.2%; Pred. No. 9.7; Matches 9; Conservative 2; Mismatches 0; Indels 5; Gaps

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Job time : 29.5882 secs

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                                                                       December 19, 2002, 16:16:27 ; Search time 9.70588 Seconds (without alignments) 36.377 Million cell updates/sec
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Sequence 4
Sequence 3
Sequence 3
Sequence 2
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Copyright (c) 1993 - 2002 Compugen Ltd.
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PCT US94-1298-1
US-08-222-851-34
US-08-21-650-20
US-08-611-650-20
US-08-611-650-20
US-08-611-650-21
PCT US94-1298-6
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US-08-105-416-16
US-08-222-851-37
US-08-222-851-36
US-08-651-650-23
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PCT-US94-12985-5
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US-08-651-650-18
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                                                   OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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58
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Match Length DB
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sednence Sed		0
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US-08-413-613-50 US-08-222-851-13 US-08-222-851-13 US-08-440-504A-5 US-08-443-650A-5 US-08-651-650-15 US-08-651-650-15 US-08-651-650-34 US-08-651-650-34 US-08-651-650-34 US-08-613-650-34 US-08-433-613-25 US-08-433-613-24 US-08-433-613-24 US-08-433-613-24 US-08-433-613-24 US-08-433-613-24 US-08-433-613-24 US-08-433-613-24 US-08-433-613-24 US-08-433-613-24	GUMENTS TING COMPOUNDS AMINO ACIDS B, NW B, NW Compound C	79/79-84 ore 58; DB 4; ed. No. 6.5e-C Mismatches
US-08-433 US-08-222 US-08-222 US-08-440 US-08-651 US-08-653	0	.84- SC Pr
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8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1  US-08-651-6  Sequence  Patent No  APPLICE  TITLE  TITLE  CORRES  COMPUTI  STABL  COMPUTI  MEDII  MEDII  MEDII  TELE	MOLECULES ORIGINAL I INDIVIT US-08-651-650 Query Match Best Local Matches 1

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US-08-222-851-33
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GENERAL INFORMATION:

APPLICANT: CLAYBE

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GENERAL INFORMATION
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE TO amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                           APPLICANT: KRENSKY, ALAN M.
APPLICANT: PARHAM, PETER
TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 10-NOV-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: University TITLE OF INVENTION: STITLE OF INVENTION: E
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                                                                       CORRESPONDENCE ADDRESS
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                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 10-NO' CLASSIFICATION:
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TOPOLOGY: li
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REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: FP
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Local Similarity 100.0%;
es 12; Conservative 0
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                                 ADDRESSEE:
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2000 PENNSYLVANIA AVENUE, NW, STE 5500
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                                                                                                                                                                                                                                                                                              CLAYBERGER, CAROL A.
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Pred. No.
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                                                                                                                                               COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PACLEASE #1.0, VE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,650
FILING DATE: 22-MAY-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MIPSAGIFICE KATE H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202) 887-1500
TELEFAX: (202) 494-0792
TELEX: 90-403 MRSMFOERSWSH
INFORMATION FOR SEQ ID NO: 33:
NEORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KRENSKY, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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APPLICATION NUMBER: US
                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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                  TELEFAX: 12.
                                                                                                     NAME: MURASHIGE, KATE H. REGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                   STREET: 2000 PENICITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tocal Similarity 60.0%; es 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 05-APR-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20006-1812
                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: MORRISUN & FURNIE, NW STREET: 2000 PENNSYLVANIA AVENUE, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YRLAIR-----RIALRY 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H: 20 amino acids amino acid
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                                                  822-0168
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                                                                                                                  29, 959
                18:
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Pred. No. 0:04
0; Mismatches
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                                                                                                         28600-20203.00
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                                                                                                                                                                                                                                                Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
0:043;
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application PC/TUS9412985
GENERAL INFORMATION:
APPLICANT: The Board of Trustees for the Leland Stanford Junior APPLICANT: University
TITLE OF INVENTION: SURFACE MEMBRANE PROTEINS AND THEIR
TITLE OF INVENTION: BFFECT ON IMMUNE RESPONSE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
                                                                                                                                                                            Query Match 75.9%; Score 44; DB 4; Length 20; Best Local Similarity 60.0%; Pred. No. 0.043; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.9%; Score 44; DB 5; Length 20; 60.0%; Pred. No. 0.043; 1ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FP-58976-PC/BIR
                                                                           MOLECULE TYPE: peptide ORIGINAL SOURCE: INDIVIDUAL ISOLATE: B2702.84-75/75-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/150,493
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND BETTAM I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: FP-58976
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                              1 YRLAIR-----RIALRY 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (415) 781-1989
(415) 398-3249
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 4 EmbarcaderCCITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: peptide PCT-US94-12985-1
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Best Local Similarity
Matches 12; Conserv
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RESULT 6

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Sequence 4, Application FC/1005712000
GENERAL INFORMATION:
APPLICANT: The Board of Trustees for the Leland Stanford Junior APPLICANT: University
ITILE OF INVENTION: SURFACE MEMBRANE PROTEINS AND THEIR
ITILE OF INVENTION: EFFECT ON IMMUNE RESPONSE
INUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-222-851-34

Sequence 34, Application US/08222851

Patent No. 5722128

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CLAYBERGER, CAROL A.
APPLICANT: FRENSKY, ALAN M.
TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8;
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                                                                                                                                                                                        ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12985
FILING DATE: 10-NOV-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/150,493
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 75.9%; Score 44; DB 5;
Best Local Similarity 60.0%; Pred. No. 0.043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: ROWland, Bertram I
REGISTRATION NUMBER: 20,015
REPRENCE/DOCKET NUMBER: FP-5;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YRLAIR-----RIALRY 12
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                          STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: siz
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

US/08/222,851

OPERATING SYSTEM: SOFTWARE: Patent:

PatentIn Release #1.0, Version #1.30

PC-DOS/MS-DOS

COMPUTER:

IBM PC compatible

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RESULT 8
US-08-222-851-35
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5723128
GENERAL INFORMATION:
                                                                              TELEPHONE: (202) 887-1500
TELEFAX: (202) 494-0792
TELEX: 90-4030 MRSUPPOERSWSH
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                     REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: CLAYBERGER, CARO
APPLICANT: KRENSKY, ALAN M.
APPLICANT: PARHAM, PETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                         CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELECTRIC (202)
                                 LENGTH: 20 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 05-AP
                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20006-1812
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TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 20 amino acids TYPE: amino acid
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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5723128
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single
linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                         05-APR-1994
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ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.2%; Score 39;
55.0%; Pred. No.
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0.36;
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                                                                                              RESULT 10
US-08-651-650-21
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                                           Sequence 21, Application US/08651650 Patent No. 6436903 GENERAL INFORMATION:
                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/08651650 Patent No. 6436903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 2006-1888

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,
               APPLICANT: CLAYBERGER, Carol A. APPLICANT: KRENSKY, Alan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CLAYBERGER, Caro
APPLICANT: KRENSKY, Alan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 12.
TELEFAX: 90-4030
                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 22-MA
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                                                                                                                                                                                                                                                                                                         INDIVIDUAL ISOLATE: B2702.84-75T/75-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                            1 YRLAIR-----RIALRY 12
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amino acid
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                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                      peptide
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                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                         67.2%;
55.0%;
IMMUNOMODULATING COMPOUNDS COMPRISING
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55.0%;
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Pred. No. 0.36;
                                                                                                                                                                                                                                           Score 39; DB 4; Length 20; Pred. No. 0.36;
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Gaps
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Patent No. 563958
GENERAL INFORMATION:
APPLICANT: Olsson, Lennart
APPLICANT: Goldstein, Avram
TITLE OF INVENTION: Class I MHC Modulation of Surface:
TITLE OF INVENTION: Receptor Activity
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flerh, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CUTY: SAR Prancisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 20;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,416
FILING DATE: 12-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REMINION BELTAM I.
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A55115-4/BIR
TELECOMMUTICATION:
TELECOMMUTICATION:
TELECOMMUTICATION:
TELECOMMUTICATION:
TELECOMMUTICATION:
TELECOMMUTICATION:
TELECOMMUTICATION:
TELECOMMUTICATION:
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: FP-58976-PC/BIR
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 781-1989
TELEFAX: 910 277299
TELEFAX: 910 277299
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acide
TYPE: amino acid
STRANDENNESS: single
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Pred. No.
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 57.99
Matches 11; Conservative
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; MOLECULE TYPE: peptide
PCT-US94-12985-6
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Best Local Similarity
Matches 6; Conserv
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ZIP: 94111
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GENERAL INFORMATION:
APPLICANT: The Board of Trustees for the Leland Stanford Junior APPLICANT: University
TITLE OF INVENTION: EFFECT ON IMMUNE RESPONSE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FIERR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                       COMPUTER: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,650
FILING DATE: 22-MAY-1996
CLLASSIFICATION: 33.6
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,950
TELEFRANCE/DOCKET NUMBER: 29,950
TELEFRANCE/DOCKET NUMBER: 20,950
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12985
FILING DATE: 10-NOV-1994
CLASSIPICATION:
  FITLE OF INVENTION: D-ISOMERS OF AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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MOLECULE TYPE: peptide

ONGINAL SOURCE:

INDIVIDIAL ISOLATE: B7202.84-75/75-84T
US-08-651-650-21
                       NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE,
CITY: WASHINGTON
STATE: DC
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/150,493
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Best Local Similarity 55.04
Matches 11; Conservative
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STRANDEDNESS: single
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RESULT 14
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                                                                                                                                              Sequence 16, Application US/08483931B Patent No. 6028171
                                                                                                                                                                                                                                                                                                                                  Query Match 60.3%;
Best Local Similarity 50.0%;
Matches 6; Conservative
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Patent No. 5853999
GENERAL INFORMATION:
                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Olsson, Lennart
APPLICANT: Goodenow, Robert S
APPLICANT: Goldstein, Avram
TITLE OF INVENTION: Class I MHC Modulation of Surface
TITLE OF INVENTION: Receptor Activity
                    TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                      APPLICANT: Olsson, Lennart
APPLICANT: Goodenow, Robert S.
APPLICANT: Goldstein, Avram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/105,416 FILING DATE: 12-AUG-1993 ATTORNEY/AGENT INFORMATION:
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   NUMBER OF SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Flerh, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Rowland, Bertram I REGISTRATION NUMBER: 200 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Methods of Screening for Agents
That Inhibit Interaction Between MHC Class I
Antigens and a Cell Surface Receptor
34
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RESULT 15
US-08-222-851-37
; Sequence 37, Application US/08222851
; Patent No. 5723128
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Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING LA...
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/028,241
APPLICATION NUMBER: 20-MAR-1987
                                                                                                           APPLICANT: CLAYBERGER, CAROL A.
APPLICANT: KRENSKY, ALAN M.
APPLICANT: PARHAM, PETER
TITLE OF INVENTION: CTTOTOXIC T-CELL LYMPHOCYTE ("CTL")
TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/483,931B FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 12-AUG-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/649,471
FILING DATE: 01-FEB-1991
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 14-MAR-1
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CITY: San Francisco
                                                  STREET:
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OPERATING SYSTEM: PC-DOS/MS-DOS
               CITY: WASHINGTON STATE: DC
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COUNTRY:
                                                                     ADDRESSEE:
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                                                  E: MORRISON & FOERSTER
2000 PENNSYLVANIA AVENUE, NW, STE 5500
USA
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Perfect score:

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Human peptide enco
Human polypeptide
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Peptide #437 encod
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Peptide #4 used in
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Immunomodulatory p
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LM609 grafted anti
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HLA-B2702 84-75-84
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Peptide #2239 e
Peptide #2351 e
Peptide #2225 e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
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                                                                     ABB132948
ABB18422
AAM51749
AAM6132
AAM26409
AAM01744
ABG35782
ABB39053
AAM72285
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ABG42100
ABG42100
AAW3786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR92911 standard; peptide; 20 AA
  95WO-US04349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0222851
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  WPI; 1995-358582/46.
                                                WO9526979-A1
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  AAR92911;
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  Immunomodulating d
HLA B2702 84-79-84
Peptide B2702-84-7
Immunomodulating d
Peptide #2275 enco
Peptide #2307 enco
Protein #2216 enco
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Human bone marrow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                               December 19, 2002, 16:02:26; Search time 28.5882 Seconds (without alignments) 55.932 Million cell updates/sec
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| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1880.DAT:*
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                                                                                                                                                                                                                                        473727
           GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                          OM protein - protein search, using sw model
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AAR33798
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Gapop 10.0 , Gapext 0.5
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Matches 11;
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dimer peptide of the invention. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or exterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR83061-R83085, AAR83090-R83096 and AAR92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
                                                                                                                                                                                                                                                                                     Claim 16;
                                                                                                                                                                                                                                                                                                                                                     New immunomodulating dimer peptide(s) - based on alpha-1 domain, used for preventing rejection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beulow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                     autoimmune
                                                                                                                                                                                                                                                                               Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clayberger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                 represents a specifically claimed immunomodulating
                                                                                                                                                                                                                                                                                  35; 41pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-US08689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dimer; immunosuppressant drug; CTL activation;
autoimmune disease; Class I HLA-B alpha-1 domain;
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Pred. No.
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                                                    compounds comprise amino acid sequences related to a Class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
Sequence
   20 AA;
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Matches Query Match Local 1 YRLLI----RYRLAIR 12 YRLAIRLNERYRLAIR 11; Conser Conservative 70.7%; 0, Score 41; I Pred. No. 0. Mismatches BB 19; Length 20 Indels 4 Gaps

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RESULT 3
AAR95429
ID AAR9
AC ACAC
ACC
ACC
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CC COMU
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CC CCOMU
CC CCOMU
CC CCC
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CC HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation; Synthetic cytolysis; HLA-B2702 84-79-84 palindrome 12-NOV-1996 AAR95429 standard; peptide; 12 AA. antigen (first entry) presenting cell.

Clayberger C, 10-NOV-1993; 10-NOV-1994; 18-MAY-1995 WO9513288-A1 (STRD ) UNIV LELAND STANFORD Krensky 93US-0150493 94WO-US12985 ¥ JUNIOR

WPI; 1995-194027/25

CC AAR95413, and AAR95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the CC HLA-B2702 8479-84 palindrome. These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane CC protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. CC p14 is found in a limited number of cell types, but is particularly CC expressed on B and T cells. p74 can be isolated by lysis of a suitable CC column containing a covalently bound HLA-B2702 palindromic peptide. CC Column containing a covalently bound HLA-B2702 palindromic peptide. CC Compositions comprising the extracellular fragment of p74 combined with CC CMB0581008 (See AAR95416), induces calcium influx, and inhibits CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate CC compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and containing the amount of binding between the candidate compound and Compsns. comprising lymphoid surface membrane proteins inhibit cytolytic activity and differentiation of CTLs. Page English.

m

12 AA;

Sequence

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immunomodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = 10 (R aa76-77) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D. S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise anino acid sequences related to a Class I HiA-B alphal domain (positions or any peptide type bond within the tytotoxic T-lymphocytes (CTL) from anino acid sequences related to a Class I HiA-B alphal domain (positions or used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in captivate CTLs. They can also inhibit the proliferation of T cells in captomate anti-CD3. The peptide can be used for preventing rejection of transplants or for transing auttoimmune diseases, e.g. diabetes, response to anti-CD3. The peptide can be used for preventing artheritis and lupus erythematosis. The products can also be the custom and diagnosis.
                                                                                                                                                                                 1;
p74... Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases
                                                                                                                                                                                 ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide B2702.84-79/79-84 tested for immunomodulating activity.
                                                                                                                                            Length 12;
                                                                                                                                                                                 Indels
                                                                                                                                                                                 ٦;
                                                                                                                                          DB 16;
                                                                                                                                        54.3%; Score 31.5; D 66.7%; Pred. No. 14; tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clayberger C, Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                        AAW33798 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 19; 41pp; English.
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                                                                                                                                                                                 8; Conservative
                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                    1 YRLLIRYRLAIR 12
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1 YRLAIR-RIALR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-086530/08.
                                                                                                   12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                   AAW33798;
                                                                                                     Sequence
                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                       RESULT 4
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This sequence represents a specifically claimed immunomodulating
dimer peptide of the invention. A peptide-type compound or variant is
claimed which has immunomodulating activity, including the N-terminal
caylated and/or C-terminal amidated or esterified forms of up to 60
amino acids, where the peptide-type compound comprises the formula; A-B,
where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or
V; aa77 = L), S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = E
Aydrophobic or small amino acid. The sequence in the brackets may optionally be
absent or truncated at any peptide type bond within the brackets. The
compounds comprise amino acid sequences related to a Class I HLA-B
alphal domain (positions 79-84). They can be used to inhibit cytotoxic
T-lymphocytes (CTL) from undesirably attacking cells in a host or in
vitro. They can also be used in combination with antigenic peptides or
proteins of interest to activate CTLs. They can also inhibit the
cused for preventing rejection of transplants or for treating autoining
the second of transplants or for treating autoining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
                                     Gaps
                                                                                                                                                                                                                                                                                                        Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
                                   1;
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   Length
                                   Indels
 DB 19;
                                   2; Mismatches
 Score 31.5; 1
Pred. No. 14;
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                                                                                                                                                                                       AAW33799 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                         [mmunomodulating dimer peptide #3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating autoimmune diseases
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                                   8; Conservative
                                                                    1 YRLLIRYRLAIR 12
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Query Match
Best Local Similarity
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Best Local Similarity
                                                                                      12 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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                                   Matches
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AAW33799
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Gaps

1;

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Query Match
Best Local S
Matches 7
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26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.
                                                                                                          agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                Sequence
                                                                                                                                                                                                                                          bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical expression analysis is useful for assessing the toxicity of chemical
                                                                                                                                                                                                                                                                                                                           The invention relates to a spatially-addressable set of single exonuncial acid probes for measuring gene expression in a sample derived mean breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #2275 encoded by breast cell single exon nucleic acid probe.
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       spatially-addressable set of single exon nucleic acid probes, ful for measuring gene expression in sample derived from humar ast, comprises number of single exon nucleic acid probes -
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                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 12592; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                 28
   Conservative
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                53.4%;
70.0%;
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 1:
                Score 31;
Pred. No.
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   Mismatches
                                   DB 22;
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                                Length 28;
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RESULT 8
ABB20217
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Best Local
                                                                                                                                                                                                                                                   The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exor nucleic acid probe of the invention.
                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                            Claim 27; SEQ ID NO 27436; 639pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-2000;
27-SEP-2000;
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03-AUG-2000;
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26-MAY-2000;
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ABB20217;
                         ABB20217 standard; Protein; 28
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; foetal liver; gene expression; single exon nucleic acid probe.
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                                                                                                                                      l Similarity
7; Conserv
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                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                        Conservative
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2000US-0236359
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2000US-0632366.
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                                                                                                                                                    53.4%;
70.0%;
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                                                                                                                                                   Score 31;
Pred. No.
                                                                                                                                        Mismatches
                                                                                                                                                    DB
43;
                                                                                                                                                               22; Length 28;
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                                                                                                                                        Indels
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23-JAN-2002

(first entry)

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; SEQ ID NO: 27708; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                    Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM67990 standard; Protein; 28 AA.
                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                    Chen W,
                                                                                                                                  26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
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26-MAY-2000, 2000US-0207456.
30-UJN-2000; 2000US-069408.
03-AUG-2000; 2000US-023366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
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    WO200157275-A2
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                                        09-AUG-2001
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                                                                                                                                                                                                                                                                                                                    Penn SG,
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Matches
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  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21515-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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Protein #2216 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single exon nucleic acid probes for analyzing gene expression in human hearts -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                      Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 15; SEQ ID No 21987; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W, Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                              2000US-0608408.
2000US-0632366.
2000US-0234687.
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04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-488899/53
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1 RLLIFYSLAV 10
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                                                                                                                                                         WO200157274-A2.
                                                                                                                  Homo sapiens
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21-SEP-2000;
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26-MAY-2000;
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0632366.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234559.
04-OCT-2000; 2000GB-0024263.
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                                                                                   27;
                                                                                                                            genome-derived single exon nucleic acid probes useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which are derived from genomic sequences expressed in the human arrow. They can be used to measure gene expression in bone marrow s, which may enable the improved diagnosis and treatment of cancers s lymphoma, leukaemia and myeloma. The present sequence is a n encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 7; Conserv
                                                                                                                                                                                                                MOLECULAR DYNAMICS
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                                                                                                            gene
                                                                                    SEQ
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                                                       invention relates to human single exon nucleic acid probes
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expression in human bone marrow -
                                                                                                            expression
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                                                                                 No 20631; 487pp; English.
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70.0%;
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                                                                                                              human cervical
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression; cervical epithelial cell;
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                                                                                                            epithelial
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see'AAI10068-AAI28459).

AAI10068-AAI28459). The present sequence is a peptide encoded probe. The SENPs are derived from human HeLa cells. The SENPs to produce a single exon microarray which are best to produce a single exon microarray which are

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Conservative

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30-JUN-2000;
03-AUG-2000;
                                                                          The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not specification, but was obtained in electronic for at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefor useful in grading and/or staging of diseases of the cervix, notably cervical cancer.
                                                                                                                                             Claim 27; SEQ ID No 28583; 654pp; English.
                                                                                                                                                                   Human genome-derived single exon nucleic aci analyzing gene expression in human placenta
                                                                                                                                                                                                                           Penn
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27-SEP-2000;
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                                                                 human genetic disorders.
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Similarity 7; Conserv
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; 2000US-0608408.
; 2000US-0632366.
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2000US-0236359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; placenta;
           53.4%;
70.0%;
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70.0%;
                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by probe for measuring placental gene
                                                                                                                                                                                                                                                 INC
           Score 31;
Pred. No.
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Pred. No.
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         DB
43;
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                                                                                                                                                                              acid
                      22;
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                                                                                                                                                                              probes useful
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                      28;
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Human peptide encoded by genome-derived single exon probe SEQ ID 27190.

(first entry)

19-AUG-2002

ABG37525;

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The present invention relates to novel single exon nucleic acid probes (see AA10010-AA110067). The present sequence is a peptide encoded by one such probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a predicting, diagnosing, staging, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
                                                                                                                                 Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  breast disease and non-carcinoma tumours.
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel single exon nucleic acid probe used to measuring gene expression in a human breast -
                                                                                                Peptide #2225 encoded by probe for measuring breast gene expression.
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AAM03543 standard; Protein; 28 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC.
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2000US-0632366.
2000US-0234687.
2000US-0236359.
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04-OCT-2000; 2000GB-0024263.
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                                                               09-OCT-2001 (first entry)
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-476286/51
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21-SEP-2000;
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung; comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method in the above mentioned microarray; assigning exons to a single exon tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of the exons in the sistence and contact of the exons in the tissues and/or cell types using hybridisation cell types indicates that the exons a new indicates that the exons a new indicates that the exons a new indicates that the exons and the and a single exon and the account of the exons in the tissues and/or cell types indicates that the exons and exons in the tissues and/or cell types indicates that the exons and expense and the account of the exons in the tissues and or cell types indicates that the exons a new exons and the account of the exons and the account of the exons and the account of the
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                                                                                                                                             Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; asrcoidosis; pulmonary haemosiderosis; pulmonary histicoytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spatially-addressable set of single exon nucleic acid probes, used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-2000; 2000US-207456P.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632468.
21-SEP-2000; 2000US-234687P.
27-SEP-2000; 2000US-23559P.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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Gaps

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ABG37525 standard; Peptide; 28 AA.

RESULT 14 ABG37525

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic
                                                                     The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID NO 15882; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-514838/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
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Note: The sequence data for this patent did not form part of the printed
                                                 treatment of cancer, leukaemia, nervous system disorders,
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                         inflammation
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Sequence
                          specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
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Matches 5
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les 5; Conserv
1 YRLLIRY 7
                Conservative
                       53.4%;
71.4%;
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Search completed: December 19, 2002; 16:19:09 Job time: 29.5882 secs

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Scoring table:

Minimum DB Maximum DB

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Q8vvt4 staphylococ
O50691 borrelia bu
Q95m82 equus cabal
O78795 pylaiella 1
Q9p1c8 homo sapien
P89006 mumps virus
P89009 mumps virus
                                                                                            09x9e7 uncultured
09x9e8 uncultured
09x9e9 uncultured
09x9f0 uncultured
099b10 human immun
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SEQUENCE FROM N.A.
MEDLINE-88072081; PubMed=2825414;
Huismans H., Cloete M., le Roux A.;
Huismans H., Cloete M., le Roux A.;
"The genetic relatedenes of a number of individual cognate genes of viruses in the bluetomgue and closely related serogroups.";
Virology 161:421-428(1987).
EMBL, M22442; AAA42841.1; -.
SEMEL, M22442; AAA42841.1; -.
SEMEL, M2242; AAA42841.1; -.
SEQÜENCE 35 AA; 4186 MW; C7E02BAA0510DFF5 CRC64;
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Q8XG89,
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative inner membrane protein (Hypothetical protein STY3241).
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Pred. No. 28;
0; Mismatches 4; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
Serotype-specific antigen (S2) RNA, 5' end (Fragment).
Bluetongue virus.
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09X9E3
09X9E4
09X9E4
09X9E6
09X9E7
09X9E8
09X9E8
09X9E8
09X9E9
09X9E9
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2.2468 8; Conservative
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QBXG89 salmonella
QBX268 escherichia
P75731 escherichia
QBx017 catla catla
QBx017 catla catla
QBX018 salmonella
QBXC5 bacillus ha
QBYC01 aeropyrum p
QBYC01 aeropyrum p
QBYC01 mumps virus
QBYC01 mumps virus
QBYC01 mumps virus
QBYC01 mandena sp
QBX254 halobacteri
QBX254 halobacteri
QBX264 uncultured
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                                                                                                                                                               December 19, 2002, 16:14:32; Search time 21.1765 Seconds (without alignments) 116.760 Million cell updates/sec
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                           GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                      671580 segs, 206047115 residues
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Maximum Match 1008
Listing first 45 summaries
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Q91KG89
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Q8V5G5
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1: sp archea:*
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58
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MEDLINE=21534947; PubMed=11677608;
Parkhill J. Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Conmerton P., Cronin A., Davis P., Davise R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi (T18.";
Nature 413:888-852(2001).
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Delius H., Darai G., Fluegel R.M.;

"DNA analysis of insect iridescent virus

permutation and terminal redundancy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chilo iridescent virus
Viruses; dsDNA viruses,
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      SEQUENCE
                                     Med. Microbiol. Immunol.
[3]
                                                                                                                                                                  MEDLINE=86174607; Pub
Lorbacher de Ruiz H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10488;
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Salmonella typhimurium,
Salmonella typhi
                                                                                                                                                                                                                                      SEQUENCE
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3 AA; 4954 MW; 5489F054F09E2277 CRC64;
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Schnitzler P., Soltau J.B., F
Delius H., Darai G.;
"Molecular cloning and physic
iridescent virus type 6: furt
the viral genome.";
Virology 160:66-74(1987).
                                                                                                                                                   "Identification of the primary structure and the codi the genome of insect iridescent virus type 6 between coordinates 0.310 and 0.347 (7990 bp)."; Intervirology 37:287-297(1994).
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=94353641; PubMed=8073636;

MEDLINE=94353641; PubMed=8073636;

Sonntag K.C., Schnitzler P., Koonin E.V., Darai G.;

Sonntag K.C., Schnitzler P., Koonin E.V., Darai G.;

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Virus Genes 8:151-158(1994).
                                                                                                                                                                                                                                                                                                                                                                         Schnitzler P., Hug M., Handermann M., Janss Delius H., Darai C., "Identification of genes encoding zinc fing chromosomal HMG protein homologue, and a puin the genome of Chilo iridescent virus."; Nucleic Acids Res. 22:158-166(1994).
SEQUENCE FROM N.A. MEDLINE=98141693;
Bahr U., Tidona C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93260401; PubMed-8492091; Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.; Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.; "Identification of the gene encoding the major capsid protein insect iridescent virus type 6 by polymerase chain reaction."; J. Gen. Virol. 74:873-879(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification and mapping DNA sequences of the genome Virus Genes 6:19-32(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of the third origin of insect iridescent virus type 6.";
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MEDLINE=92196996; PubMed=1549908;
"`~~^~~mann M. Schnitzler P., Rosen-Wolff
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                                                                                              Koonin E.V.,
                                                                                                         Schnitzler P.,
                                                                                                                       MEDLINE=94292906;
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                              MEDLINE=95213160; PubMed=7698884;
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                                                    iridescent virus type 6 encodes a subunit of eukaryotic RNA polymera Virol. 75:1557-1567(1994).
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  PubMed=9482589; A., Darai G.;
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nntag K.C., Muller
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01-MAY-2000 (TEMBLrel. 13, Created)
01-MAY-2000 (TEMBLrel. 13, Last sequence update)
01-MAY-2000 (TEMBLrel. 20, Last annotation update)
01-MAR-2002 (TEMBLrel. 20, Last annotation update)
01-MAR-2002 (TEMBLrel. 20, Last annotation update)
01-MAR-2002 (TEMBLrel. 20, Last annotation update)
Catla catla (catla).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Cyprinidae; Catla.
NCBI_TAXID=72446;
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                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                         01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
From BASES 685948 to 696574 (Section 60 of 400) of the complete
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Pred. No. 2.8e+02;
2; Mismatches 3; Indels
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Pred. No. 3.2e+02;
4; Mismatches 1; Indels
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Smbl, ABC00170; AAC73766.1; -.
Complete proteome.
SEQUENCE 39 AA; 4865 MW; 8CABSA9ED57CD6F1 CRC64;
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54.5%;
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STRAIN=K12 / MG1655;
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NCBI_TaxID=562;
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MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
May and T., Markino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama M., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                           Jakob N.J., Muller K., Bahr U., Darai G.;
"Analysis of the First Complete DNA Sequence of an Invertebrate
Iridovirus: Coding Strategy of the Genome of Chilo Iridescent Virus.";
Virology 286:182-196(2001)
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"The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101 and 0.391, similarities in coding strategy between insect and vertebrate iridoviruses."; Virus Genes 15:235-245(1997).
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MEDLINE=99383793; PubMed=10456793;
Muller K., Tidona C.A., Darai G.;
"Identification of a gene cluster within the genome of Chilo
iridescent virus encoding enzymes involved in viral DNA replication
                                                                                        SEQUENCE FROM N.A.
MEDLINE=99125223; PubMed=9926400;
Muller K., Tidona C.A., Bahr U., Darai G.;
Miletrication of a thymidylate synthase gene within the genome of Chilo iridescent virus.";
Virus Genes 17:243-258(1998).
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Pred. No. 2.4e+02;
4; Mismatches 2; Indels
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Pred. No. 2.8e+02;
2; Mismatches 3; Indels
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF303741; AAK82175.1; --
SEQUENCE 53 AA; 6610 MW; 6C206BDEFA37C3B8 CRC64;
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MEDLINE=21342589; PubMed=11448171;
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Best Local Similarity 54.5%;
Matches 6; Conservative ;
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Virus Genes 18:243-264(1999)
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
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            Delius H., Darai G.; "Molecular cloning and physical mapping of the genome of insect iridescent virus type 6: further evidence for circular permutat
                                                                                                                                                                                              Delius H., Darai G., Fluegel R.M.; "DNA analysis of insect iridescent virus permutation and terminal redundancy.";
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Viruses; dsDNA viruses, no R
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Hypothetical
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MEDLINE=21534948; PubMed=11677609;

MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.

Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

Waterston R., Wilson R.K.;
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                                                MEDLINE=87321126; PubMed=2820141;
Schnitzler P., Soltau J.B., Pischer M.,
                                                                         SEQUENCE FROM N.A.
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Lorbacher de Ruiz H., Gelderblom H.,
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   Virus
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MEDLINE=98141693; PubMed=9482589;

Bahr U., Tidona C.A., Darai G.;

"The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101 and 0.391; similarities in coding strategy be insect and vertebrate iridoviruses.";
                                                                                                                                                                                                                                 Sonntag K.C., Schnitzler P., Janssen W., Darai G.;
"Identification of the primary structure and the codi
the genome of insect iridescent virus type 6 between
coordinates 0.310 and 0.347 (7990 bp).";
                                                                                                                                                                                                                                                                                                                                             Sonntag K.C., Schnitzler P., Koonin E.V., Darai G.; "Chilo iridescent virus encodes a putative helicase belonging distinct family within the 'DEAD/H' superfamily: implications
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"Identification of genes encoding zinc fin
chromosomal HWG protein homologue, and a pr
in the genome of Chilo iridescent virus.";
Nucleic Acids Res. 22:158-166(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterization of the third origin of insect iridescent virus type 6.";
                                                                                                                        "Insect iridescent virus type 6 encodes a polypeptide largest subunit of eukaryotic RNA polymerase II.";
J. Gen. Virol. 75:1557-1567(1994).
                                                                                                                                                          Schnitzler P., Sonntag
Koonin E.V., Darai G.;
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                                                                                                                                                                                                                                                                                                                       evolution of large DNA viruses.";
Virus Genes 8:151-158(1994).
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Darai G.;
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                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                   MEDLINE=95213160;
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Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Mauda S., Fuhahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi T., Tanaka T., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H., "Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix KI.";
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"Genetic heterogeneity of mumps virus in the United Kingdom:
identification of two new genotypes.";
J. Infect. Dis. 180:829-833 (1999).
EMBL; AF147761; AAD54491.1;
Interpro; IPR001477; SH.
Probom; PD001504; SH; 1.
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Pred. No. 6.2e+02;
2; Mismatches 3; Indels
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Mumps virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
NCBI TaxID=11161;
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InterPro; IPR001211; PhospholipaseA2.
PROSITE; PS00118; PA2-HIS; UNKNOWN.1.
Hypothetical protein; Complete profesome.
SEQUENCE 54 AA; 6140 MW; 7579866613EACFIC CRC64;
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                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAX-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein APES036.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                           54 AA
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MEDLINE=99367591; PubMed=10438373;
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NCBI_TaxID=56636;
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18 LIIRFRL 24
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"Analysis of the First Complete DNA Sequence of an Invertebrate
Iridovirus: Coding Strategy of the Genome of Chilo Iridescent Virus.";
Virology 286:182-196(2001).
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EMBL, AP001512; BAB05345.1; Hypothetical protein; Complete proteome.
SEQUENCE 53 AA; 6234 MW; 343F2BA731F5E63C CRC64;
                                                                                                                                                                         MEDLINE=99383793; PubMed=10456793; MEDLINE=99383793; PubMed=10456793; Muller K., Tidona C.A., Darai G.; "Identification of a gene cluster within the genome of Chilo iridescent virus encoding enzymes involved in viral DNA replication
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MEDLINE=99125223; PubMed=9926400;
Muller K., Tidona C.A., Bahr U., Darai G.;
"Identification of a thymidylate synthase gene within the genome
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NCBI_TaxID=86665;
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40.0%; Pred. No. 5.5e+02;
iive 5; Mismatches 1; Indels
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Submitred (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF303741; AAR82033.1; -.
SEQUENCE 50 AA; 5601 MW; C3390D2D93B68010 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein BH1626.
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STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed=11058132;
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                                                                                                                                                                                                                                                                                                                                   and processing.";
Virus Genes 18:243-264(1999)
                                                                                               Chilo iridescent virus.";
Virus Genes 17:243-258(1998)
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Best Local Similarity
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27 KILLKIRLAV 36
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Q8V5G5;
O1-MAR-2002 (TrEMBLrel. 20, 0
O1-MAR-2002 (TrEMBLrel. 20, 1
O1-JUN-2002 (TrEMBLrel. 21, 1
Small hydrophobic protein.
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Q9J4L2;
01-OCT-2000
         Tecle T., Bottiger B., Orvell C., Johansson B.;
"Characterization of two decades of temporal co-circulation of four mumps virus genotypes in Denmark, including one new genotype.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF365883; AAL68449.1; -.
InterPro; IPR001477; SH.
                                                                               STRAIN=V79-49863;
                                                                                                              Paramyxoviridae;
NCBI_TaxID=11161;
                                                                                                                            Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Rubulavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amexis G., Chumakov K.;
"Quantitative analysis of sequence diversity in Jeryl Lynn mumps vaccine live.";
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Clarke D.K., Sidhu
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Paramyxoviridae; Paramyxovirinae; Rubulavirus
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PF01445; SH; 1
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                                                                                                                                                                                                                                                                                                                                                            Length 57;
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RESULT 15
Q8X254
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Q8YKB6
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

WEDLINE-21595285; PubMed=11759840;

WEDLINE-21595285; PubMed=11759840;

Waneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasam Watanabe A., Iriguchi M., Ishikawa A., Kawashima K. Kishida Y., Kohara M., Matsumoto M., Matsumo A., M. Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Y. Yasuda M., Tabata S.;

"Complete genomic sequence of the filamentous nitro;
"DNA Res. 8:205-213 (2001).
                                                                                                                                                                                                                             Q8X254
Q8X254;
01-MAR-2002
                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, C
01-MAR-2002 (TrEMBLrel. 20, I
01-MAR-2002 (TrEMBLrel. 20, I
Hypothetical 3.6 kDa protein
Halobacterium volcanii (Halof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anabaena sp. (strain PCC /120).
Plasmid pCC7120alpha.
Bacteria; Cyanobacteria; Nostocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD001504; SH; 1. SEQUENCE 57 AA; 6844 MW;
                                   Submitted (NOV-2001) to the EMBL; AF454092; AAL57845.1;
                                                                      "Differential expression of genes using RNA arbitrarily primed PCR i
                                                                                                                                                                 Archaea;
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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ASR7385.
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01-MAR-2002
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SEQUENCE
                                                              volcanii.
                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                     NCBI_TaxID=2246;
                                                                                                                                                    Halobacteriaceae;
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             Hypothetical
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5; Conserv
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                                                                                                                                                                Euryarchaeota;
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31 AA;
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                      protein.
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Μ¥.
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                                                                                                                                                                                          (Fragment)
                                                                                                                                                                                                                                                                                                                                                                               Score 27; DB 16;
Pred. No. 6.2e+02;
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Pred. No. 6.2e+02;
682119419273C9D0 CRC64;
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Muraki A.,
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ö 0; Gaps Query Match 44.8%; Score 26; DB 1; Length 31; Best Local Similarity 45.5%; Pred. No. 5.5e+02; Matches 5; Conservative 3; Mismatches 3; Indels

1 YRLLIRYRLAI 11 || || :: | : 1 YRRLIKHALEL 11 ઠે g

Search completed: December 19, 2002, 16:21:56 Job time : 22.1765 secs

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RESULT 1
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                                                                                                                                               December 19, 2002, 16:03:12; Search time 5.47059 Seconds (without alignments) 90.980 Million cell updates/sec
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P80024
P05949
O83397
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P35306
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                  GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                112892 seqs, 41476328 residues
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WY PETWA
CPRF CANPG
VPU HVAA2
Y382 TREPA
Y18 ARCFU
VSH MUNPB
HSPI PONPY
LITO1 HORVU
LITO1 HORVU
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LCRT YERPS
Y195 BPY7
Y573 TREPA
PYY AMICA
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HSP1_ALOSE
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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58
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Match Length DB
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.

MEDLINE=86056972; PubMed=3934047;

Cully D.F., Garro A.J.;

"Nucleotide sequence of the immunity region of Bacillus subtilis

bacteriophage phi 105: identification of the repressor gene and its

Gene 38:153-164(1985).
                                                                                                                                                                                                                                                                                                                                                                               Bacteriophage phi-105.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klebsiella pneumoniae.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Klebsiella.
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              P19719
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PIR; 024521; IMBPB.
Hypothetical protein.
SEQUENCE 44 AA; 5574 MW; C440D1B134841832 CRC64;
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ID YFHA KLEPN

AC P217I0,

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein in GLNB 5'region (Fragment).
                                                                                                                                                                                                                                                                                                                                      01-WAR-1989 (Rel. 10, Last sequence update) 01-MAR-1989 (Rel. 10, Last annotation update) Hypothetical immunity region protein 8.
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Pred. No. 25;
3; Mismatches
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ATP8 COTURA
VSH MUMP1
VSH MUMPE
VSH MUMP2
VSH MUMP4
BUK CLOPE
BUK CLOPE
RL18 HALME
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01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last seq
01-MAR-1989 (Rel. 10, Last ann
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                                                                                                                                                                                                                                                                                           STANDARD;
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   Viruses, dsDNA viruse
Lambda-like viruses.
NCBI TaxID=10717;
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LLLRYFRLALK 19
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Best Local Similarity
NCBI_TaxID=573;
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SEQUENCE FRC
STRAIN=M5a1;
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P80024;
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InterPro; IPRO2078; Sig54_interact.
PROSITE; PS00675; SIGMAS4_INTERACT_1; PARTIAL.
PROSITE; PS00676; SIGMAS4_INTERACT_2; PARTIAL.
PROSITE; PS00688; SIGMAS4_INTERACT_3; PARTIAL.
PROSITE; PS00468; SIGMAS4_INTERACT_4; PARTIAL.
PROSITE; PS50045; SIGMAS4_INTERACT_4; PARTIAL.
Hypothetical protein; Sensory transduction; Phosphorylation;
Transcription regulation; DNA-binding; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for content partities removed.
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Schwartz T.W.;
                                                                                                                                                                                                                                                            TISSUE=Intestine;
MEDLINE=91301137;
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Crania
Petromyzontiformes; Petromyzontidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pancreatic polypeptide MY (PMY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQÜENCE
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mol. Gen. Genet. 215:134-138(1988).
-!- FUNCTION: PROBABLE MEMBER OF A TWO-COMPONENT REGULATORY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of the Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89201233;
                                                                                                                         from lamprey intestine.";
Eur. J. Biochem. 199:293-
                                                                                                                                                                     tyrosine,
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7757;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Petromyzon marinus (Sea lamprey)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holtel A., Merrick M.
    InterPro;
                                                                                                                                                                "Primary structure and conformational analysis of cyrosine, a peptide related to neuropeptide Y and
                                                                                                                                                                                                                                                                                                                  EQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
                                               SIMILARITY: BELONGS; S16943; S16943;
                                                                                              J. Biochem. 199:293-298(1991)
SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: THE CENTRAL REGION CONTAINS A SI INTERACTION ATP-BINDING DOMAIN. SIMILARITY: TO EQUIVALENT PROTEIN IN E.COLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS. SIMILARITY: THE CENTRAL REGION CONTAINS A SIGMA-54 FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YFHA/YFHK
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  IPR001955; Pancreatic_hormn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                   PubMed=2070789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=2907369;
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                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Hyperoartia;
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Mismatches
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peptide
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RESULT 5
VPU_HV1A2
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CPRP_CANPG
  RRA RA
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P05949;
01-NOV-1988
SEQUENCE FROM N. ....
MEDLINE=85090453; PubMed=2578227;
Sanchez-Pescador R., Power M.D., Barr
Sanchez-Pescador R., Stanton Brown-Shimer S.L., Gee
                                                                                            υđΛ
                                                                                                                                                                                                                                                                                                            Neuropeptide; Horn SEQUENCE 38 AA;
                                                                                                                                                                                                                                                                                                                                                                            hormone (CHH)
pagurus.";
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99025664; PubMed=9809792;
Chung J.S., Wilkinson M.C., Webster S.G.;
Chung J.S., Wilkinson M.C., Webster S.G.;
"Amino acid sequences of both isoforms of crustacean hyperglycemic hormone (CHH) and corresponding precursor-related peptide in Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
CHH precursor related peptide (CPRP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPRP
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SMART; SM00309; PAH; 1
                                                                    Human immunodeficiency virus type 1 (ARV2/SF2 isolate)
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                     VPU protein
                                                                                                                01-NOV-1988
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                             Regul. Pept. 77:17-24(1998).
-!- TISSUE SPECIFICITY: PRODUCED BY THE MEDULLA TERMINALIS
THE EYESTALKS AND TRANSPORTED TO THE SINUS GLAND WHERE
                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Sinus gland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P81033;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00265; PANCREATIC_HORMONE_1; PROSITE; PS50276; PANCREATIC_HORMONE_2;
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                                                        NCBI_TaxID=11685
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brachyura; Eubrachyura; Cancroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cancer pagurus (Rock crab)
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                                   FROM N.A.
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                                                                                                     protein).
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annotation update)
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Pred. No.
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76E5D50BED01B90A
                                                                                                                                                                                                                                                                           Score 25; DB 1;
Pred. No. 1.1e+02
                                                                                                                                                                                                                                                                                                            C979C87EE31ABB90 CRC64;
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on update)
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  Steimer K.S., Renard A., Re
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42 IRYRL 46
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                                                                                                                                                             Y718 ARCFU
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P28082;
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VSH MUMPB
ID VSH M
AC P2808:
DT 01-AUC
DT 01-NOU
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                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstantion the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                     ö
                                       Science 227:484-492(1985).
-!- FUNCTION: ACTS IN THE DEGRADATION OF CD4 IN THE ENDOPLASMIC RELICULOM AND IN THE ENHANCEMENT OF VIRION RELEASE FROM THE PLASMA MEMBRANE OF INFECTED CELLS.
-!- SUBCELLULAR LOCATION: Membrane-bound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Praser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey B.K., Clayton R., Ketchum K.A., Sodergren B., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.,
Levy J.A., Dina D., Luciw P.A.;
"Nucleotide sequence and expression of an AIDS-associated retrovirus
                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                        Score 25; DB 1; Length 38; Pred. No. 1.1e+02; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spirochaetales; Spirochaetaceae; Treponema.
                                                                                                                                                                                                                                                                                                               7F6431F505BED6C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein TP0382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 AA.
                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Nichols;
MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE001217; AAC65383.1; -.
TIGR; TP0382; -.
                                                                                                                                                                                                                               EMBL; K02007; AAB59881.1; -.
HIV; K02007; VPU$SF2.
                                                                                                                                                                                                                                                                                                                                         43.1%;
                                                                                                                                                                                                                                                                                                             38 AA; 4390 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 281:375-388(1998).
                                                                                                                                                                                                                                                       InterPro; IPR002094; Vpu.
Pfam; PF00558; Vpu; 1.
Transmembrane; AIDS.
                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 50.0
المالية 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                              3 LLIRYRLAIR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spirochete."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98049343; PubMed-989475; Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Deterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou Coverbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
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Length 40;
                                                           1; Indels
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Hypothetical protein; Complete proteome.
SEQUENCE 46 AA; 5271 MW; 3AC6F5E54D58F9C5 CRC64;
Score 25; DB 1; I
Pred. No. 1.1e+02;
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Last annotation update)
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                                                              4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE001055; AAB90531.1; -.
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16-0CT-2001 (Rel. 40, Last seq
16-0CT-2001 (Rel. 40, Last ann
   43.18;
44.48;
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در 5، Conservative
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                                                           4; Conservative
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Query Match
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19 LVRHRLTMQ 27
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Best Local
                                                            Wyckoff G.J., Wang W., Wu C.-I.;
Wyckoff G.J., Wang W., Wu C.-I.;
"Rapid evolution of male reproductive genes in the descent of man."
Nature 403:304-309(2000).

-i- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN O
SPERM DURING THE HAPLOID PHASE OF SPERWATOGENESIS. THEY COMPACT
SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
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SEQUENCE
                                                                                                                                                                                                                               MEDLINE=94141943; PubMed=8308910; Retief J.D., Winkfein R.J., Dixon Ballabriga J., Oliva R.;
                                                                                                                                                                                                                                                                                                                                                          Sperm PRM1.
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"Identification of a new mumps virus lineage by nucleotide
analysis of the SH gene of ten different strains.";
Arch. Virol. 128:371-377(1993).
            : :
                                                                                                                                                   MEDLINE=20123244; PubMed=10659848; Wyckoff G.J., Wang W., Wu C.-I.:
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                 Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
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01-FEB-1994 (Rel. 28, Last seq
15-JUN-2002 (Rel. 41, Läst ann
Sperm protamine P1 (Cysteine-r
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Paramyxoviridae; Paramyxovirinae; Rubulavirus
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                         SUBUNIT: CROSS-LINKED BY INTERCHAIN DISULFIDE DNA-HELIX (BY SIMILARITY). SUBCELLULAR LOCATION: NUCLEAR. CTISSUE SPECIFICITY: TESTIS.
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6814 MW;
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Last annotation update)
ysteine-rich protamine).
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Pred. No. 2.1e+02;
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B8F2F917B4A8EF3C CRC64;
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TIO1 RESULT 10 밁 Ş Best Loc Matches Query Match 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last sanotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last sequence update)
16-JUN-2002 (Re Testis; SPECIES=H.vulgare; STRAIN=cv. Igri;
Brown A.P.C., Dunn A.M., Goddard N.J., Hughes M.A.;
"Identification of a novel low-temperature-response element in promoter of the barley gene lt101.1.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. LT01 HO Q42509; EMBL; L14589; AAA36946.1; -.
EMBL; AF215710; AAF34623.1; -.
InterPro; IPR000221; Protaine P1. Goddard N.J., Dunn A.M., Zhang L., White A.J., "Molecular analysis and spatial expression pat temperature-specific barley gene, blt101.", plant Mol. Biol. 23:871-879(1993). NCBI\_TaxID=4513, use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). the This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -Gulick P.J., Shen W., An H.;
"ESI3, a stress-induced gene from Lophopyrum elongatum."; SPECIES=L.elongatum; TISSUE=Root; MEDLINE=94211914; PubMed=8159795; SPECIES=H.vulgare; STRAIN=cv. Igri; TISSUE=Meristem; MEDLINE=94072734; PubMed=8251639; SEQUENCE FROM N.A. HORVU Chromosomal PROSITE; Fram; This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way -!- SIMILARITY: BELONGS SEQUENCE FROM N.A. SEQUENCE FROM N.A. 42 Local თ European RYRLRCR RYRLAIR HORVU PF00260; protamine P1; 1. TE; PS00048; PROTAMINE P1; 1. DNA condensation; Nuclear protein. T 0 BY SIMILARITY. E 50 AA; 6660 MW; D9935BF411E5BE78 Similarity 5; Conser pean Bioinformatics Institute. Ti non-profit institutions as long protein; Nucleosome core; Spermatogenesis; Conservative 12 STANDARD; 4588; 41.48; 71.48; TO THE UPF0057 (PMP3) 0; Score 24; DB Pred. No. 2.3e 0; Mismatches 54 There 2.3e+02; 2; B pattern protein are no res FAMILY. CRC64; Length Jack (Salt-stress induced of. Indels (Potential). .L., Hu a lowrestrictions 50 DNA-binding; Hughes M.A.; 0 Gaps g 9 its 0

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(See http://www.isb-sib.ch/announce/

Usage by

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Bacteriophage T7
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ID LCRT YERPS
AC Q00932;
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
Triticeae, Hordeum
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Pred. No. 2.5e+02;
4; Mismatches 2; Indels
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52521C3946B8BBF2 CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Low temperature induced protein lt101.2.
modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
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                                          EMBL; Z25537; CAA80984.1; -.
EMBL; AJ310994; CAC37081.1; -.
EMBL; U00966; AAA21847.1; -.
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Pfam; PF01679; UPF0057; 1.
PROSITE; PS01309; UPF0057; 1.
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Pfam; PF01679; UPF0057; 1.
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Transmembrane.
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33.38;
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54 AA; 5936 MW;
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T7-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rimpilaeinen M., Forsberg A., Wolf-Watz H., "An novel protein, LcrQ, involved in the low-calcium response of Yersinia pseudotuberculosis shows extensive homology to YopH.", J. Bacteriol. 174:3355-3363(1992).
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"Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 energy elements.";
J. Mol. Biol. 166:477-535(1983).
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41.4%; Score 24; DB 1; Length 56;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels
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                                                                                                                                                01-JUL-1993 (Rel. 26, Last sequence update) 01-JUL-1993 (Rel. 26, Last annotation update) Low calcium response locus protein T.
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21-JUL-1986 (Rel. 01, Last sequence update)
01-MAR-1989 (Rel. 10, Last annotation update)
Hypothetical gene 19.5 protein.
56 AA
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InterPro; IPR001230; Prenyl_site.
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MEDLINE=83241725; PubMed=6864790;
                                                                                          01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last seq
01-JUL-1993 (Rel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                          Tersinia pseudotuberculosis.
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STANDARD;
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32 YRLLRYYK 39
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A195_BPT7
A195_BT7
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RESULT 15
PYY AMICA
ID PYY AMICA
AC P29205;
DT 01-DEC-1992
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15-DEC-1998
15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayron R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; V01146; CAA24443.1; -. PIR; A04429; Q9BPE7. PIR; S42341; S42341.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Complete proteome. SEQUENCE 30 AA; 3380 MW; COB2640A4B30E33C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001232; AAC65550.1; -. TIGR; TP0573; -.
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Science 281:375-388(1998).
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MEDLINE=98332770; PubMed=9665876;
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Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
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                                                                                                                                                                                                                                                                                                            Local Similarity
les 3; Conserv
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L protein TP0573.
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Pred. No. 2.1e+02;
4; Mismatches 2
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There are no restrictions on its long as its content is in no way moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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Matches 5
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MEDLINE-91296574; PubMed-2067973;
Conion J.M., Bjenning C., Moon T.M., Youson J.
"Neuropeptide Y-related peptides from the panc
[eel], holostean (bowfin) and elasmobranch (s)
L Peptides 12:221-226(1991).
C -i- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
PYY.
                                                                                            Hormone; Amidation.
MOD_RES 36
SEQUENCE 36 AA;
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15-JUN-2002 (Rel.
Peptide YY-like (F
                                                                                                                              PROSITE; PS00265; PANCREATIC_HORMONE_1; PROSITE; PS50276; PANCREATIC_HORMONE_2;
                                                                                                                                                                ProDom;
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Pfam; PF00159; hormone3; 1.
                                                                                                                                                                                                                                                                                                                                                            Amia calva (Bowfin).
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii;
                                                                                                                                                        SMART; SM00309; PAH;
                                                                                                                                                                  PRINTS; PR00278; PANCHORMONE. ProDom; PD001267; Pancreatic_
                                                                                                                                                                                                                 HSSP; P01303; 1RON.
                                                                                                                                                                                                                                                                                                                            SEQUENCE
 17
                      4 LIRYRLAIR 12
 LARYYTALR
                                              Similarity
5; Conser
                                                                                            36 AA; 4333 MW;
                                               Conservative
25
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                                                                                                                                                               Pancreatic_hormn; 1.
                                                                                                          36
                                                         39.7%;
                                              Score 23; DB 1;
Pred. No. 2.6e+02;
1; Mismatches 3
                                                                                            AMIDATION.
56B46F3C08666671 CRC64;
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                                                                                                                                                                                                                                                                                         Youson J.H.,
                                                                                                                                                                                                                                                                             pancreas
                                                                                                                                                                                                                              PYY FAMILY
                                                                                                                                                                                                                                                                  pancreas of a teleostean
(skate) fish.";
                                                                    Length 36;
                                               Indels
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Search completed: December 19, 2002, 16:19:46
Job time: 6.47059 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

December 19, 2002, 16:16:02; Search time 10.4118 Seconds (without alignments) 110.799 Million cell updates/sec Run on:

US-08-653-294C-42 58 1 YRLLIRYRLAIR 12 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

15911

Minimum DB seq length: 0 Maximum DB seq length: 60

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

pir 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	7.124 4.84 1.094 7.194 7	44000000 040000000	. 4400000	110 AH0876 IMB8 G35926 G90716 G64801 B83853	conserved hypothet hypothetical immun T-cell receptor ga probable RNA (impohypothetical prote hypothetical prote hypothetical prote hypothetical prote
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U 4 1 U U U U U U U U U U U U 1 N D 4 4 4 4 4 4 4 4 4 4	. 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		10100000000000	C82714 SHNZBF A05012 A05012 PD0006 S42781 B82184 S72280 S72280 B89903 F82816	45 F 10 4

hypothetical prote	integral membrane	hypothetical prote	gene 19.5 protein	relaxin - baboon (	hypothetical prote	hypothetical prote	relaxin - hamadrya	hypothetical prote	probable succinate	pancreatic hormone	hypothetical prote	hypothetical prote	ribosomal protein	gene 39.2 protein	hypothetical prote
G82593	168744	H82409	Q9BPE7	S42785	I58970	C71309	156451	G81597	S42876	PCGS	T16051	E86007	875680	D45731	S66584
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## ALIGNMENTS

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conserved hypothetical protein STY3241 [imported] - Salmonella enterica subsp. enterica Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001 C;Accession: AH0876 B;Parkhili, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seron A;Reference number: AB0502; PMID:11677608 A;Status: preliminary A;Molecule type: DNA A;Cross-references: GB:AL513382; PIDN:CAD02912.1; PID:g16504165; GSPDB:GN00176 C;Genetics: A;Gene: STY3241

ö Gaps ö Score 30; DB 2; Length 43; Pred. No. 49; 1; Mismatches 3; Indels Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative

## 1 YRLLIRYRLAI 11 ઠે

22 YGLLSRLRIAI 32 d

hypothetical immunity region protein 8 - Bacillus phage phi-105
C.Species: Bacillus phage phi-105
A.Note: host Bacillus subtilis
A.Note: host Bacillus subtilis
C.Space: 2.0-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Aug-1999
C.Accession: G2421
R.Cully, D.F.; Garro, A.J.
Gene 38, 153-164, 1985
A.Title: Nucleotide sequence of the immunity region of Bacillus subtilis bacteriophage; A.Reference number: A91535; MUID:86056972; PMID:3934047

A,Molecule type: DNA A,Residues: 1-44 <CUL> A;Cross-references: GB:M11920; NID:g215477 C;Comment: This is the hypothetical translation of a sequence that was not reported as

7 Gaps 1; DB 4; Length 44; 0; Indels Query Match
49.1%; Score 28.5; D
Best Local Similarity 63.6%; Pred. No. 99;
Matches 7; Conservative 3; Mismatches Children and

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C;Accession: G64801

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                    hypothetical protein b0669 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: G64801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 8, 11-22, 2001
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A:Reference number: A99629; MUID:21156231; PMID:11258796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T-cell receptor gamma chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 30-Jun-2001
C;Accession: S35926
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
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A; Residues: 1-39 < HAY>
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gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable RNA [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C;Species: Escherichia coli
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A; Residues: 1-25 < MAT>
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A;Accession: S35926
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R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah. awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ki DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: F72675
                                                                                                                                                                                      A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-54 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein APES036 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: F72675
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A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B83853
                                                                                                                                                                                                           A;Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79806.1; A;Experimental source: strain K1
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A;Molecule type: DNA
A;Residues: 1-53 <STO>
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change
C;Accession: B83853
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A; Residues: 1-39 <BLAT>
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6; Conservative
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Pred. No. 2.4e+02;
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Pred. No. 1.1e+02;
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small hydrophobic protein - mumps virus

Query Match
Best Local Similarity 50.0%;
Matches 5; Conservative 5

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hypothetical protein BBH36 - Lyme disease spirochete plasmid H/lp28-3
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
C;Accession: B70239
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whitc son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
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A;Experimental source: strain B31
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C; Species: mitochondrion Pylaiella littoralis
C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 03-Jun-2002
C; Accession: 709464
R; Rousvoal, S; Oudoc, M; Fontaine, J; Kloareg, B; Goer, S.L.
J; Mol. Biol. 277, 1047-1057, 1998
A; Title: Witnessing the evolution of transcription in mitochondria: The mitochondrial ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuropeptide Y - sea lamprey
Cispecies: Petromyzon marinus (sea lamprey)
Cjate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
CjAccession: 816843
R;Conlon, J.M.; Bjornholm, B.; Jorgensen, F.S.; Youson, J.H.; Schwartz, T.W.
R;Conlon, J.M.; Bjornholm, 1991 1991
A;Title: Primary structure and conformational analysis of peptide methionine-tyrosine,
A;Reference number: 816943; MUID:91301137; PMID:2070789
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55.6%; Pred. No. 2.5e+02;
tive 2; Mismatches 2; Indels
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Pred. No. 3.4e+02;
2; Mismatches 3; Indels
                                                       Indels
Pred. No. 1.8e+02;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.8%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: pancreatic hormone
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 55.6
Matches 5; Conservative
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 1-36 <CON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 YYLIIFYRPSI 46
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Best Local Similarity
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17 LSKYMLAVR 25
                                                                                                                                                                                                                       |:|| |: |
11 YKLLSRHEL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 LIRYRLAIR 12
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                                                                                                                                                     1 YRLLIRYRL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: S16943
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
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A.Note: Note: Nostco sp.
A.Note: Note: No
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A,Residues: 1-26 <HOL>
A,Cross-references: EMBL:X14012; NID:g43804; PIDN:CAA32176.1; PID:g43805
C,Superfamily: nitrogen assimilation regulatory protein ntrC; response regulator homolog
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C; Date: 07-Um-1990 #sequence_revision 07-Jun-1990 #text_change 26-Aug-1999
C; Accession: S04376
R; Holtel, A.; Merrick, M.
Mol. Gen. Genet. 215, 134-138, 1988
Mol. Gen. Genet. 215, 134-138, 1988
A; Title: Identification of the Klebsiella pneumoniae glnB gene: nucleotide sequence of A; Reference number: S04376; MUID:89201233; PMID:2907369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transposase asr7385 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha
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                                      Species: mumps virus
Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
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Pred. No. 2.5e+02;
2; Mismatches 3; Indels
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6; Conservative

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2 RLLIRYRLAI 11

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Best Local Similarity Matches 6; Conserv

A;Gene: asr7385 A;Genome: plasmid Query Match DB 2; Length 26; 44.8%; Score 26;

Query Match

(m - %

THE PERSON

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R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
Nature 390, Smith, H.O.; Venter, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi. A; Reference number: A70100; MUID:98065943; PMID:9403685
A; Accession: A70237
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R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.: Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
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A;Cross-references: GB:AE000784; NID:g2690041; PIDN:AAC66020.1; PID:g2690076; TIGR:BBH1 A;Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein BBH16 - Lyme disease spirochete plasmid H/lp28-3
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
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A;Accession: B81006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein NMB2097 [imported] - Neisseria meningitidis (strain MC58 serogroup C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
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A;Residues: 1-55 <ROU>
A;Cross-references: EMBL:AF034976; NID:g3243103; PID:g3243105
A;Experimental source: strain Roscoff
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                                                         A; Molecule type: DNA
A; Residues: 1-40 < KLE>
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A; Residues: 1-29 <TET>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Cross-references: GB:AE002559; GB:AE002098; NID:g7227357; PIDN:AAF42414.1; PID:g72273
;Experimental source: serogroup B, strain MC58
                                                                                                             Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                            Accession: A70237
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Best Local &
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Pred. No. 3.2e+02
3; Mismatches
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Pred. No.
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Query Match
Best Local Similarity 60.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps

Qy 2 RILIRYRLAI 11
Db 20 QVLKRYLLAI 29
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Search completed: D Job time : 11.4118

December 19, 3 secs

2002, 16:23:00

Human peptide enco HLA-B2702 84-79-84 Peptide B2702.84-7

Immunomodulating d Rice B2F protein f Tachytegrin and/or Human interleukin-Human immune/haema Novel human connec Peptide #3135 enco Peptide #3115 enco Protein #3079 enco Human brain expres Human bone marrow Peptide #3065 enco Peptide #3065 enco Peptide #3065 enco Puman peptide enco Peptide #3065 enco Puman peptide enco Peptide #3065 enco Human peptide enco Peptide #3065 enco Immunomodulatory p Immunomodulatory p Immunomodulatory p

Peptide fragment o Alphal-helix of HL HLA-B2702.75-84(D) HLA-B2702 CTL modu HLA-B2702 CTL modu HLA-B2702 CTL modu

Human Class I HLA-

T-cell modulating T-cell modulating Cytomodulating lip

Perfect score:

Sequence:

1

OM protein

Run on:

Scoring table:

Minimum DB Maximum DB

Database

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Human; prostate cancer antigen; cytostatic; uropathic; diagnostic; reproductive system; chromosomal marker; forensic; urinary disorder; chronic nephritis; blood-related disorder; thrombosis.
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                                                                          AAW33799
AAY32166
AAW23775
AAB88757
ABB53194
AAM91292
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ABB30484
ABB31080
AAB21080
AAM56467
AAM16667
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AAM04383
AAW33782
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04-FEB-2000; 2000US-0180628.
02-MAR-2000; 2000US-0184664.
02-MAR-2000; 2000US-018974.
17-MAR-2000; 2000US-0190776.
18-APR-2000; 2000US-0190776.
19-PAY-2000; 2000US-0209467.
28-UJN-2000; 2000US-0209467.
28-UJN-2000; 2000US-0209467.
  17-JAN-2001; 2001WO-US01328
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  WO200155316-A2
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                   GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                 908470 seqs, 133250620 residues
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Listing first 45 summaries
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Human bone marrow

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Result

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14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 11-JUL-2000; 14-JUL-2000; 26-JUL-2000;

26-JUL-2000; 14-AUG-2000; 07-JUL-2000; 07-JUL-2000; 11-JUL-2000;

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     20-OCT 2000

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08-NOV 2000

17-NOV 2000

17-NO
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disorders
and also f
The invention relates to novel isolated human prostate cancer antige polynucleotides (I) and polypeptides (II). (I) and (II) are useful f preventing, treating or ameliorating a medical condition when administered. (I), (II) and the antibody to (II) are useful for treapreventing and/ or prognosing disorders related to the reproductive system including prostate cancers; urinary disorders e.g. chronic nephritis; and blood-related disorders e.g. thrombosis. (II) can be
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N-PSDB; AAS40225.
                                                                                                                                                Claim
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2000US-0251988
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                                                                                                                                                                            for treating, preventing and/ or prognosing the reproductive system including prostate and detection e.g. diagnosis -
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                                                                                                                                              English.
                                                                                       cancer antigen
) are useful for
                                                     for treating,
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2000US-0216647 2000US-02174880 2000US-0217487 2000US-02217487 2000US-022964 2000US-022953 2000US-0225213 2000US-0225266 2000US-0225266 2000US-0225275 2000US-0225759 2000US-0225759

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22-AUG-2000; 2000US-0227182.
33-AUG-2000; 2000US-0227009.
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02-OCT-2000;
02-OCT-2000;
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                                                                                                                                                                                                                                                                                                                         Human; reproductive system related antigen; reproductive system disorder;
for testing and detection e.g. as a chromosomal marker and in forensics. (1) and the anti-(11) antibody can be used in testing and detection in amunoassays. AAU22702-AAU22913 represent the human prostate cancer antigen amino acid sequences, and related amino acid sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at: ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                    Gaps
                                                                                                                                    ;
                                                                                                            Score 34; DB 22; Length 49;
Pred. No. 33;
2; Mismatches 3; Indels
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Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                       1 RIALRYRILLRY 12
                                                                                                                                                                    :||| | :|| |
14 QIALSYNLLLLY 25
                                                                                                                                                                                                                                                                                                                                     cancer; gene therapy
                                                                                       49 AA
                                                                                                                                                                                                                                                                                                                                                                              WO200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
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26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens,
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                                                                                                                                                                                                                                                        AAM96170;
                                                                                       Sequence
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RESULT 3
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Best Local
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01-DEC-2000
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05-DEC-2000
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
colony stimulating factor; hormone; angiogenic factor.
         Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1; HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral; anti-fusogenic; differentiation factor; interleukin; interferon;
                                                      Core
                                                                                                AAY88733;
                                                                                                                    AAY88733 standard;
                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-465570/50.
                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-DEC-2000;
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17-NOV-2000;
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17-NOV-2000;
                                                                           23-MAY-2000
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                                                                                                                                                                        14 QIALSYNLLLLY 25
                                                                                                                                                                                                                 Local Similarity
nes 7; Conserv
                                                                                                                                                                                          1 RIALRYRILLRY 12
                                                   polypeptide fragment T No.
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                                                                                                                                                                                                                                                                                                                                        SEQ
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                                                                                                                                                                                                                   Conservative
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2000US-0249210.
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                                                                          (first
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2000US-0251868
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2000US-0249218
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                                                                                                                                                                                                                                                                                                                                       NO 4828; 1297pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                             SC,
                                                                                                                    peptide; 38
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                                                                          entry)
                                                                                                                                                                                                                             58.6%;
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                                                                                                                                                                                                                             Score 34;
Pred. No.
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                                                      88
                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                               33;
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                                                                                                                                                                                                                                       Length 49;
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RESULT 4
ABB00092
ID ABBC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
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                               Modified-site
                                                                                                                                                                                                      Viridiae
                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
                                                                                                                                                                                                                                                                                                                                                                                                     Viral DP178/107-like region peptide T88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB00092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB00092 standard; Peptide; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprises enhancer sequence
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                                                                                                    Modified-site
                                                                                                                                                                                                                                                                    infection
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24 LAVREKVLIRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38
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                                  38
                                                                                                                                    Location/Qualifiers
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/note= "C-terminal amide"
                                                                  note=
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45.5%;
                                                                  "N-terminal is substituted
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Pred. No. 38;
5; Mismatches
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The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107 correspond to amino acids 618-673 (heptad repeat region HR2) and 558-555 (heptad repeat region HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a compound that inhibits the formation of or disrupts a DP10/7/DP178 complex, especially compounds with antifusogenic, antivixal or intracellular modulatory activity, by detecting the formation of a DP107/DP178 complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to peptides which exhibit anti-retroviral
   Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus 1 isolate
                                                                             Disclosure; Page 188; 587pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DP178-like/DP107-like peptide T-88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU12641 standard; Peptide; 38 AA.
                                                                                                                                                                                                                                                                                                                                                                                  56.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                             the specification.
                                                                                                                                                                                                                                                                                                                                                38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 IALRYRILLRY
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24 LAVREKVLIRY
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                                           infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-673 (heptad repeat region HR2) and 558-555 (heptad repeat region HR1) respectively, of HIV-11A1 transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other normal infectivity of viruses such as RSV and HIV. The heptad normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in
                                                                                                                                                                                                                                                                 Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV; virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
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                                                                                                                                                                                            Lambert DM,
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                                                                                                                                                                                            Erickson JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viral core polypeptide, SEQ ID NO: 84.
                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 34; 587pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB01557 standard; Peptide; 38 AA.
                                                                           07-FEB-2001; 2001WO-US03988
                                                                                                            29-FEB-2000; 2000US-0515965
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                                                                                                                                                                                        Antczak JB, Delmedico MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antczak JB, Delmedico MK,
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                                                                                                                                                  (TRIM-) TRIMERIS INC
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24 LAVREKVLIRY 34
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les 5; Conserv
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WO200164013-A2.
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Best Local S
Matches 5
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                      The present sequence is a core polypeptide which may be linked to an enhancer peptide to form a novel hybrid polypeptide. The hybrid polypeptide exhibits enhanced pharmacokinetic properties relative to those exhibited by the core polypeptide when introduced into a living system. It is used to increase the in vitro or ex vivo half-life of the core polypeptide. The hybrid and core polypeptides can be used for the core polypeptide. The hybrid and core polypeptides can be used for modulating fusognic events and intracellular processes involving
                                                                                                                                                                                                                                                                                   Disclosure; Page
                                                                                                                                                                                                                                                                                                                                                                               New hybrid polypeptide, e.g. viral infections, o
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   coiled-coil peptide interactions. Other uses include preventing,
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45.5%;
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07-MAR-1997;
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11-APR-1997;
11-APR-1997;
11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modulation of neurotransmitter exchange and sperm-egg fusion), intracellular processes involving colled-coll peptides (e.g. bacterial infections) and viral infections that involve cell-cell and/or virus-cell fusion (e.g. viral infections caused by human immunodeficiency virus, respiratory syncytial virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and polio virus).

The enhancer peptide sequence increases the half-life and reduces the clearance rate of therapeutic peptides, which increases their efficacy and minimises the incidence and severity of adverse side effects. In addition, this increases the sensitivity of the diagnostic procedure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis; neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; testis; tumour; foetal brain ti fusion protein; cancer; central nervous system; seizure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein encoded by
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24 LAVREKVLIRY 34
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22-AUG-1
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22-AUG-1
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22-AUG-1
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This sequence represents a secreted human protein encoded by the nucleic acid molecule designated Gene 79 from the human cDNA clone HSKNE46 (deposited as clone ATCC 209046).

The gene can be used to generate flusion proteins by linking to the gene con be used to generate flusion proteins by linking to the gene can be used to generate flusion proteins by linking to the gene con the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAVS9511-V59812; amino acid sequences AAV3731-W75026) which are useful for preventing, treating or ameliorating medical conditions eap by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the presence of mutations in the my polymucleotides. Based on which tissues they are most highly expressed in (see AAV59511 for described uses).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human brain expressed single exon probe encoded protein SEQ ID NO: 33122.
                                                                                                                                                                 New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                               Ebner R, Endress GA;
Greene JM, Hu JS;
Dlsen HS, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
epilepsy; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.2%; Score 32; DB 19; Length 39; 77.8%; Pred. No. 59;
                              Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, I
Ferg P, Ferrie AM, Fischer CL, Florence KA, Greene JM,
Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS,
Ruben SM, Shi Y, Soppet DR, Young PE, Yu CL, Zeng Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                      Claim 1; Page 674; 721pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM61017 standard; Protein; 54 AA.
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30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632466.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001; 2001WO-US00667.
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nes 7; Conservative
                                                                                                                 WPI; 1998-506364/43.
N-PSDB; AAV59742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 39 AA;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                        Human; bone marrow expressed microarray; cancer; leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The
The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow
                                               Example 4;
                                                                   Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human bone marrow -
                                                                                                       WPI; 2001-488900/53.
                                                                                                                              Penn
                                                                                                                                                                           04-OCT-2000;
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27-SEP-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                               SEQ ID NO:
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; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                            leukaemia;
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70.0%;
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                                               34020; 658pp + Sequence Listing;
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                                                                                                                                                                                                                                                                                                                                                           exon; gene expression analysis; probe;
a; lymphoma; myeloma.
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                                                                                                     The present invention relates to single exon nucleic acid probes (SENP: see ARI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                            Penn
                                                                                                                                                                                                                                                                                                                                           30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                      Sequence
                                                                                                                                                                           Claim 27; SEQ ID No 34169; 654pp; English.
                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                     21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; microarray; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide #7937 encoded by probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM33900;
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1 RIALRYRILL 10
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                                                                                            genetic disorders.
                     l Similarity
7; Conserv
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; placenta; antenatal diagnosis;
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                                   55.2%;
70.0%;
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                       Score 32; DB Pred. No. 83; 2; Mismatches
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Pred. No. 83;
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from hunan lung comprising single exon nucleic acid probes having one of from hunan lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes, the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the hunan lung; measuring gene expression in a sample derived from hunan lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the array; identifying exons in a eukaryotic genome, comprising of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included to anying a fragment identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in the tissues and/or cell types using hybridisation to a single exon comprising one microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene; particularly expression analysis, and for identifying exons in a gene; particularly
                                                                                                                                      Human peptide encoded by genome-derived single exon probe SEQ ID 33256.
                                                                                                                                                                                                                                                                      Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                  Human; single exon probe; asthma; lung cancer; COPD, ILD, chronic Obstructive pulmonary disease; interstital lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          measure gene expression in human lung samples -
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ABG43591 standard; Peptide; 54 AA.
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21-SEP-2000; 2000US-234687P.
27-SEP-2000; 2000US-236359P.
04-OCT-2000; 2000GB-0024263.
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2000US-0608408.
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                                                                                         19-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                         hyaline membrane disease.
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                                             ABG43591;
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using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease.

(COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary dulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension cand hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention.

Note: The sequence data for this patent did not form part for the printed specification, but was obtained in electronic format directly from WIPO at format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; rcell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
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Pred. No. 83;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR95429 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Page 12; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLA-B2702 84-79-84 palindrome.
                                                                                                                                                                                                                                                                                                                                          55.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94WO-US12985.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clayberger C, Krensky AM;
                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                         1 RIALRYRILL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 RLALLHRILL 33
                                                                                                                                                                                                                                                                                                     54 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9513288-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAY-1995.
                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR95429;
                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
AAR95429
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RESULT 14
AAW33798
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Best Local
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                                                                           Peptides AAW33784-98 and AAW33778-9 were assayed for their immunomodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84= a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and as represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HLA-B alphal domain (positions 19-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from the brackets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA-B2702.60-84 (see AAR95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity or T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.
                                                         undesirably attacking cells in a host or in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 19; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New immunomodulating dimer peptide(s) - based alpha-1 domain, used for preventing rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-086530/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide B2702.84-79/79-84 tested for immunomodulating activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW33798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW33798 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RIALRYRILLRY 12
                                 in combination with antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clayberger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0653294
They can also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Krensky AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
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Pred.
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No. 21;
                                 peptides or proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on a Class I HLA-B of transplants or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۲.
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                                 They can also be 
eins of interest to
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RESULT 15
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         V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytocoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                        dimer peptide of the invention. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Page 35; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   treating autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                     New immunomodulating dimer peptide(s) - based alpha-1 domain, used for preventing rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-086530/08.
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                                                                                                                                                                                                                                                                                                                               This sequence represents a specifically claimed immunomodulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beulow R, Clayberger C, Krensky AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunomodulating dimer peptide #3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (STRD ) UNIV LELAND STANFORD JUNIOR
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8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0653294.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dimer; immunosuppressant drug; CTL activation;
autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.3%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31.5; I
Pred. No. 21;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                     a Class I HLA-B
transplants or
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SQ Seguence 12 AA;

Ouery Match 54.3%; Score 31.5; DB 19; Length 12; Best Local Similarity 66.7%; Pred. No. 21; Matches 8; Conservative 2; Mismatches 1; Indels 1; Gaps

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Query Match Length DB

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                                                                      RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Ra Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Ra Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Bartons M.R.S., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M., RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El Dorry H., RA Fraga J.S., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., RA Fraga J.S., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., RA Fraga J.S., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., Marchado M.A., Madeira A.M., B.N., Madeira H.M.F., Martino C.L., RA MacChado M.A., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Nanii A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., RA Manii A. Jr., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., RA de Silva A.M., C., de Sa R.G., Santelli R.V., Sawasaki H.E., RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., RA Vallada H., Van Sluys M.A., Verjovski-Almeids S., Vettore A.L., RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.,
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01-MAY-2000
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A receptor.",
Hypertension 25:694-698(1995).
Hypertension 18 AA; 2137 MW; 61026B2DA726629B
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Mammalia; Eutheria;
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                         genome sequence of the plant re 406:151-159(2000).
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Rodentia;
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Sciurognathi; Muridae;
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        Med.
                                                                               Delius H., Darai G., Fluegel R.M.; "DNA analysis of insect iridescent virus permutation and terminal redundancy.";
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G.
Fuji F., Hirama C., Nakamura Y., Ogasawara
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI
                                                                                                                                      Chilo iridescent virus
Viruses; dsDNA viruses,
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01-DEC-2001
                                                                                                                                                                                                                                                                                                                             Hypothetical SEQUENCE 51
                                                                                                                                                                                                                                                                                                                                                      halodurans and genomic sequence comparison Nucleic Acids Res. 28:4317-4331(2000).
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STRAIN=C-125 / JCN
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                 in mice."
                                    MEDLINE=86174607;
Lorbacher de Ruiz
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                           "Insect iridescent
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H., Gelderblom H., Hofmann
t virus type 6 induced toxic
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26 MW; 2D3382F1E200B2AD CRC64;
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        175:43-53 (1986)
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                                                                                                                                                                                                                                                                                                                                  MEDLINE=93118242; PubMed=1475907; Sonntag K.C., Darai G.; Sonntag K.C., Darai G.; Medication of the third origin of DNA replication of the genome of insect iridescent virus type 6."; Virus Genes 6:333-342(1992).
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                                                                                                                                MEDLINE=89073752; PubMed=3201750; Fischer M., Schnitzler P., Delius H., Darai G.; Identification and characterization of the repetitive DNA element in the genome of insect iridescent virus type 6."; Virology 167:485-496(1988).
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Sonntag K.C., Schnitzler P., Koonin E.V., Darai G.;
"Chilo iridescent virus encodes a putative helicase belonging to a
distinct family within the 'DEAD/H' superfamily: implications for the
evolution of large DNA viruses.";
Virus Genes 8:151-158(1994).
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MEDLINE=22196996; PubMed=1549908;
Handermann M., Schnitzler P., Rosen-Wolff A., Raab K., Sonntag K.C.,
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           MEDLINE=87321126; PubMed=2820141; Scholz J., Scholz J., Schitzzler P., Soltau J.B., Fischer M., Reisner H., Scholz J., Deliuu H., Darai G.; "Molecular cloning and physical mapping of the genome of insect infederent virus type 6: further evidence for circular permutation the viral genome."; Virology 160:66-74(1987).
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Sonntag K.C., Schnitzler P., Janssen W., Darai G.;
Identification of the primary Structure and the coding capacity
the genome of insect tiridescent virus type 6 between the genome
coordinates 0.310 and 0.347 (7990 bp).";
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MEDLINE=93260401; PubMed=8492091;
Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.;
Stohwasser R., Rab K., Schnitzler P., Janssen W., Darai G.;
Ildentification of the gene encoding the major capsid protein insect iridescent virus type 6 by polymerase chain reaction.";
J. Gen. Virol. 74:873-879(1993).
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MEDLINE=94167241; PubMed=8121799;
Schnitzler P., Hug M., Handermann M., Janssen W., Koonin B.V.,
Delius H., Darai C.;
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SEQUENCE FROM N.A.
MEDLINE=98141693; PubMed=9482589;
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SEQUENCE FROM N.A.
MEDLINE=21342589; PubMed=11448171;
Jakob N.J., Muller K., Bahr U., Darai G.;
Jakob N.J., Muller K., Bahr U., Darai G.;
"Analysis of the First Complete DNA Sequence of an Invertebrate
Iridovirus: Coding Strategy of the Genome of Chilo Iridescent Virus.";
Virology 286:182-196(2001).
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
Bahr U., Tidona C.A., Darai G.; "The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101 and 0.391; similarities in coding strategy between insect and vertebrate iridoviruses.";
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STRAIN=CV. INBRED LINE Q66;
MEDLINE=21238656; PubMed=11340182;
MEDLINE=21238656; PubMed=11340182;
Mitochondrial aldehyde dehydrogenase activity is required for male fertility in maize.";
Plant Cell 13:1063-1078(2001).
EMBL; AF318133; AAK60511.1;
InterPro; IPR002086; Aldehyde_dehydr.
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                                                                                                                                                                                                     MEDLINE=99125223; PubMed=9926400;
Muller K., Tidona C.A., Bahr U., Darai G.;
"Identification of a thymidylate synthase gene within the genome of
Chilo iridescent virus.";
Virus Genes 17:243-258(1998).
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Jakob N.J., Mueller K., Bahr U., Darai G.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF30741; AAK82029.1; -.
SEQUENCE 54 AA, 6581 WW; 5E8172628A363A55 CRC64;
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1-UNN-2002 (TrEMBLrel. 21, Last annotation update)
cytoplasm male sterility restorer factor 2 (Fragment).
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Virus Genes 18:243-264(1999)
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SEQUENCE 5
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Ogata H., Audic S., Renesto-Audiffren P.,
Samson D., Roux V., Cossart P., Weissenbar
Raoult D.;
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F., Cui X., Horner H.T., Weiner H., Schnable P.S.;
tochondrial aldehyde dehydrogenase activity is required for
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RESULT 10
P93387
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Matches 5
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Best Local
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01-MAY-1997
01-DEC-2001
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                                                                                                             Karrer E.B., Beachy R.N., Holt C.A.; "Cloning of tobacco genes that elicit the plant Mol. Biol. 36:681-690(1998).

EMBL; U66272; AAC49978.1; -.
SEQUENCE 60 AA; 6800 MW; 3091FAA0484CE
                                                                                                                                                                                                                                                                                                              ORF.
                                                                                                                                                                                                                                                                                                                                                                       P93387
P93387;
                                                                                                                                                                                                                                                  Nicotiana tabacum (Common tobacco).

Nicotiana tabacum (Common tobacco).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 7.1 kDa protein.
Pichia etchellsii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
SEQUENCE 60
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EMBL; AJ278986; CAC08223.1;
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NCBI_TaxID=136928;
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01-MAR-2001
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                                                                                                                                                                                                       SEQUENCE FROM N.A.
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VRYKVILWY 26
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al protein; Plasmid.
60 AA; 7129 MW; F
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idou L., Larsen M.,
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4; Mismatches
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Pred. No. 4
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4.3e+02;
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098157
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Hoelzel A.R., Stephens J.C., O'Brien S.J.;
Hoelzel A.R., Stephens J.C., O'Brien S.J.;
"Molecular genetic diversity and evolution at the MHC DQB locus in tur species of pinnipeds.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF111032; AAC96347.1; -
Remb.; AF1800353; MHC_II_beta.

Probom; PR00969; MHC_II_beta; 1.

Probom; P0006328; MHC_II_beta; 1.

NOW_TER 1 1
NOW_TER 47 47

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SEQÜENCE 47 AA; 5727 MW; OE672D7A5F436208 CRC64;
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=94114596; PubMed=8286438;
MCDILINE=94114596; PubMed=8286438;
Morozov S.Yu., Denisenko O.N., Zelenina D.A., Fedorkin O.N.,
Solovyva A.G., Maiss E., Casper R., Atabekov J.G.;
"A novel open reading frame in tobacco mosaic virus genome coding for a putative small, positively charged protein.";
Biochimie 75:659-665(1993).
SEQUENCE 39 AA; 4714 MW; 21686DIDB5B859F6 CRC64;
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Tobacco mosaic virus.
Viruses; seRNA positive-strand viruses, no DNA stage; Tobamovirus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Pinnipedia, Phocidae, Mirounga.
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Pred. No. 5.2e+02;
1; Mismatches 2; Indels
                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MHC class II antigen (Fragment).
MHC-DDB.
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                                             39 AA.
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Best Local Similarity 62.5
Matches 5; Conservative
                                             PRELIMINARY;
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Hoelzel A.R., Stephens J.C., O'Brien S.J.;
"Molecular genetic diversity and evolution at the MHC DQB locus in four species of pinnipeds.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF111034; AAC56549.1;
InterPro; IPR000353; MHC_II_beta.
ProDom; PD0065; MHC_II_beta.
ProDom; PD000328; MHC_II_beta; 1.
ProDom; PD000328; MHC_II_beta; 1.
Royoprotein; MHC_II; Transmembrane.
NON_TER 47 47
                               Mirounga leonina (Southern elephant seal).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Carnivora, Pinnipedia, Phocidae, Mirounga.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Pinnipedia, Phocidae, Mirounga.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MHC class II antigen (Fragment)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MHC class II antigen (Fragment).
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Pred. No. 5.2e+02;
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62.5%; Pred. No. 5...
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01-MAY-1999 (TrEMBLrel. 10, Created)
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REPUBLICAL A.R., Stephens J.C., O'Brien S.J.;

Hoelzel A.R., Stephens J.C., O'Brien S.J.;

Tour species of pinnipeds.";

Line pecies of pinnipeds.";

REMBL; AF111036; AAC96351.1; -.

REMBL; AF11036; AAC96351.1; -.

RILL BETAL, DEBUT DETAL, DETAL, DEBUT DETAL, 
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Best Local Similarity
Matches 5; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Mirounga.
NCBI TaxID=9715;
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10 RVRVLTRY 17
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                                                                                              December 19, 2002, 16:03:12; Search time 5.47059 Seconds (without alignments) 90.980 Million cell updates/sec
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            GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                               112892 segs, 41476328 residues
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Y10G_ECOLI

Y195_BPT7

YCUA_LACCU

VSH_MUNP2

VSH_MUNP3

VSH_MUNP3

VSH_MUNP3

VSTO HELLPY

VPU HYLA2

VY19E_BPT3

RL13_BORBU

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriophage phi-105.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
VORI_TaxID=10717;
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16-OCT-2001 (Rel. 40, Last sequence update)
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BTR; G24821; IMBP8.
Hypothetical protein.
SEQUENCE 44 AA; 5574 MW; C440D1B134841832 CRC64;
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Pred. No. 21;
2; Mismatches
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                   BFR NITWI
SPRT RAT
SX19 MOUSE
UCRY BOVIN
YOLE BPT4
LCRT YERPS
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AC P10431;
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AC Q37874;
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                  MEDLINE=96196428; PubMed=8648624; Mahdi A.A., Sharples G.J., Mandal T.N., Lloyd R.G.; Mahdi A.A., Sharples G.J., Mandal T.N., Lloyd R.G.; "Holliday junction resolvases encoded by homologous rusA genes Escherichia coli K-12 and phage 82."; J. Mol. Biol. 257:561-573(1996).
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             EMBL; X92587; CAA63322.1; -.
EMBL; AE000160; -; NOT_ANNOTATED_CDS
                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein ylcG in lambdoid DLP12 p
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16-OCT-2001
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Mahdi A.A.; Sharples G.J., Mandal T.N., Lloyd R.G.;
"Holliday junction resolvases encoded by homologous rusA genes
EcoGene;
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                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12.", Science 277:1453-1474(1997).
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by non-profit institutions as long as its content
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P35923;
01-JUN-1994
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21-JUL-1986
01-MAR-1989
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P03804;
                                                                                   01-JUN-1994 (Rel. 29, L
16-OCT-2001 (Rel. 40, L
Hypothetical 6.1 kDa pr
Lactobacillus curvatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Complete proteome. SEQUENCE 46 AA; 5493 MW; E5D339EBC756A26E CRC64;
          SEQUENCE FROM N.A. STRAIN=LTH1174;
                                                                Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                  Hypothetical SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; dsDNA 1
T7-like viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriophage
MEDLINE=94058500; PubMed=7694558;
                                         NCBI_TaxID=28038;
                                                                           Plasmid 60
                                                                                                                                                                                                                                                                                                                        PIR; S42341;
                                                                                                                                                                                                                                                                                                                                           EMBL; V01146; CAA24443.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Mol. Biol. 166:477-535(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunn J.J., Studier F.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10760;
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                                                    actobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete nucleotide sequence of bacteriophage ocations of T7 genetic elements.";
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4; Conserv
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4 (Rel. 29, Last sed)
1 (Rel. 40, Last and
1 6.1 kDa protein:
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49 AA; 5434 MW;
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71.4%;
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                                                                Lactobacillales;
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Pred. No. 1.4e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                 Pred. No. 1.
                                                                                                                                                                                                                                                                                                  FB1C9240BA465342 CRC64;
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                                                                Lactobacillaceae,
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1.5e+02;
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Tichaczek P.S., Vogel R.F., Hammes W.P.;
"Cloning and sequencing of curA encoding curvacin A, the bacteriocin produced by Lactobacillus curvatus LTH1174.";
Arch Microbiol. 160:279-283(1993).
-!- FUNCTION: HAS SOME FUNCTION IN CURVACIN A BIOSYNTHESIS, TRANSPORT OR RESISTANCE.
                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                      Score 25, DB 1; Length 51;
Pred. No. 1.5e+02;
4; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mumps virus (strain Edingburgh 2), and
Mumps virus (strain Edingburgh 6).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
                                                                                                                            Plasmid; Hypothetical protein.
SEQUENCE 51 AA; 6142 MW; B77506B2076B7CFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49121303FE0DED94 CRC64;
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Yeo R.P., Afzal M.A., Foresy T., Rima B.K.;
I'dentification of a new mumps virus lineage by nucl analysis of the SH gene of ten different strains.";
Arch. Virol. 128:371-377(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Small hydrophobic protein.
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57 AA; 6894 MW;
                                                                                                                                                                                         Query Match 43.1
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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ProDom; PD001504; SH; 1.
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PIR; S19869; SHNZE6.
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12 LALQLIIILRF 22
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P28085;
                                                                                                                                                                                                                                                                                                                                                                                                                  VSH MUMP2
P28084;
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VSH_MUMP4
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MEDLINE=93168036; PubMed=8435047;
Yeo R.P., Afzal M.A., Forsey T., Rima B.K.;
"Identification of a new mumps virus lineage by nucleotide sequence analysis of the SH gene of ten different strains.";
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Pred. No. 1.7e+02;
2; Mismatches 4; Indels
                                                                                                                                Mumps virus (strain Edingburgh 4).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
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01-AUG-1992 (Rel. 23, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Small hydrophobic protein.
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Best Local Similarity 45.5
Matches 5, Conservative
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Pfam; PF01445; SH; 1.
ProDom; PD001504; SH; 1.
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RESULT
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TRANSMEM 8
SEQUENCE 57 P
                     Hypothetical
HP0560 OR JHI
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16-OCT-2001
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16-0CT-2001
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А260_НЕГЪА
ТАТВН
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InterPro; IPR001477; SH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeo R.P., Afzal M.A., Forsey T., Rima B.K.; "Identification of a new mumps virus lineage by nucleotide sequence analysis of the SH gene of ten different strains."; arch. Virol. 128:371-377(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
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01-AUG-1992 (Rel.
01-NOV-1997 (Rel.
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01-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSH MUMPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD001504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01445;
Helicobacter pylori (Campylobacter pylori), and
                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                             Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93168036; PubMed=8435047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=11172;
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les 5; Conser
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                 P-2001 (Rel. 40, Created)
P-2001 (Rel. 40, Last sequence update)
P-2001 (Rel. 40, Last annotation update)
P-2001 (Rel. 40, Last annotation update)
P-2001 (Rel. 40, Last annotation update)
P-2001 (Rel. 40, Created)
P-2001 (Rel. 40, Last sequence update)
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                                                                                                                       STANDARD;
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6892
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45.5%;
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                                                                                                                                                                                                                                                                                           Score 25;
Pred. No.
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B8FA5B0945BC04D3 CRC64;
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B8F2F917B4A8EF3C CRC64;
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1.7e+02;
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                                                                                                                                    VPU_HV1A2
P05949;
01-NOV-1988
01-NOV-1988
01-NOV-1997
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MEDLLINE=97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Dougherty B.A.,

Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,

Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

McKenney K., FitzGerald L.M., Lee N., Peterson J.D., Kelley J.M.,

Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,

Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
SEQUENCE FROM N.A.
MEDLINE=85090453; PubMed=2578227;
Sanchez-Pescador R., Power M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G. Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., IT Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E.,
                                                                       Human immunodeficiency viviruses; Retroid viruses;
                                                                                                           ΛāΛ
                                                                                                                        VPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000570; AAD07633.1; -. EMBL; AE001484; AAD06083.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gastric pathogen Helicobacter Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria, Proteobacteria, epsilon subdivision, Helicobacter group,
                                                        NCBI_TaxID=11685;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein;
TRANSMEM 3 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trust T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99120557;
                                                                                                                                                                                                                                                                                                                                                    Local
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6; Conserv
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                                                                                                                     (Rel. 0
(Rel. 0
(Rel. 3
(U ORF
                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                 09, Created)
09, Last sequence update)
35, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                3169 MW;
                                                                                                                     protein).
                                                                                                                                                                                                                                                                                                                                                    41.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Complete proteome.
3 POTENTIAL.
                                                                            virus type 1 (ARV2/SF2 isolate) (HIV-1).
es; Retroviridae; Lentivirus.
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Pred. No.
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    Barr
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 P.J.,
                                                                                                                                      update)
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    Steimer
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Vovis
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequ. 16-OCT-2001 (Rel. 40, Last anno 50S ribosomal protein L32.
RPMF OR BBO703.
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Best Local Similarity 40.v
                              4; Conservative
                                                                                                                                                   STANDARD;
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               Best_Local Similarity
Matches 4; Conserv
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36 LGVRHRICLK 45
                                                         4 LRYRILLRY 12
                                                                        NCBI TaxID=139;
                                                                                                                                                RL32 BORBU O51646;
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     Query Match
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                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                   ö
                                       (ARV-2).";
Science 227:484-492(1985).
-!- FUNCTION: ACTS IN THE DEGRADATION OF CD4 IN THE ENDOPLASMIC
-!- FUNCTION: ACTS IN THE ENHANCEMENT OF VIRION RELEASE FROM THE PLASMA MEMBRANE OF INFECTED CELLS.
-!- SUBCELLULAR LOCATION: Membrane-bound.
Stemuien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A., Levy J.A., Dina D., Luciw P.A.; "Nucleotide sequence and expression of an AIDS-associated retrovirus
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-86209997; PubMed=3010556; Xamada K., Minagawa T.; Xamada M., Fujisawa H., Kato H., Hamada K., Minagawa T.; "Cloning and sequencing of the genetic right end of bacteriophage T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
T7-like viruses.
NCBI_TaxID=10759;
                                                                                                                                                                                                                                                                                                                                                                                  .
0
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Pred. No. 1.7e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamada M., Fujisawa H., Kato H., Hamada K., Minagawa T.;
Virology 154:246-246(1986).
                                                                                                                                                                                                                                                                                                                            7F6431F505BED6C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 AA; 5484 MW; 266E0EF6CC4B52AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-APR-1990 (Rel. 14, Last annotation update)
Hypothetical gene 19.5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 AA.
                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                        EMBL; KO2007; AAB59881.1; -. HIV; KO2007; VPG$SF2.
InterPro; IPR002094; Vpu. Pfam; PF00558; Vpu. ITransmembrane; AIDS.
                                                                                                                                                                                                                                                                                                                                                      41.4%;
40.0%;
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                                                                                                                                                                                                                                                                                                                          38 AA; 4390 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virology 151:350-361(1986).
                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; 123476; 09BPT3
Hypothetical protein
SEQUENCE 49 AA;
                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                       2 IALRYRILLR 11
                                                                                                                                                                                                                                                                                                                                                                                                                        : : || :||
26 VLIEYRKILR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriophage T3
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SEQUENCE
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Y195_BPT3
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SERANTE-27C3 5210 / B31;

MEDLINE=98065943; PubMed=9403685;

Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,

Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,

Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,

Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,

Van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,

Ulterbook T., Mathey L., McDonald L., Artiach P., Bowman C.,

Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,

Smith H.O., Venter J.C.;
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01-0CT-1996 (Rel. 34, Last sequence update)
116-0CT-2010 (Rel. 40, Last annotation update)
Hypothetical 3.5 kDa protein in YCF33-TRNY intergenic region (ORF29A).
Odontella sinensis (Marine centric diatom).
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-1- SIMILARITY: BELONGS TO THE L32P FAMILY OF RIBOSOWAL PROTEINS.
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Score 24; DB 1; Length 49;
Pred. No. 2.3e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 24, DB 1; Length 59;
Pred. No. 2.8e+02;
4; Mismatches 2; Indels
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Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
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Last annotation update)
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RESULT 15
LHG_RHOVI
ID LHG_RHOVI
AC P04126;
DT 20-MAR-1987
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                                                                                                       Query Match
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20-MAR-1987 (Rel. 04, Last sequence update)
01-NOV-1991 (Rel. 20, Last annotation update)
Light-harvesting protein B-1015, gamma chain.
Rhodopseudomonas viridis.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Hyphomicrobium group; Blastochloris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae; Biddulphiophycidae; Eupodiscales; Eupodiscaceae; Odontella. NCBI_TaxID=2839;
                                                                                                                                                                                                                                                                                              Biol. Chem. Hoppe-Seyler 366:87-98(1985).
-!- FUNCTION: ONE OF THE COMPONENTS OF THE BACTERIOCHLOROPHYLL-PROTEIN COMPLEX IN THE CHROMATOPHORE MEMBRANE.
PIR; A03455; LBRFGV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z67753; CAA91683.1; --
Chloroplast; Hypothetical pu
SEQUENCE 29 AA; 3481 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia
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Kowallik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Frei "The chloroplast genome of a chlorophyll a+c-containing alga, Odontella sinensis.";
                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                Antenna complex; Light-harvesting polypeptide.
VARIANT 34 34 T -> V (IN 33% OF THE MOLECULES).
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=85225948; PubMed=389089;
Brunisholz R.A., Jay F., Suter F., Zuber H.;
"The light-harvesting polypeptides of Rhodopseudomonas viridis. The
complete amino-acid sequences of B1015-alpha, B1015-beta and B1015-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1079;
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31
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1; Mismatches
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Search completed: December 19, 2002, 16:19:45 Job time : 5.47059 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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1 RIALRYRILLRY 12 US-08-653-294C-41 58 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

15911 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 60

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

RESULT 1
IMBEV Junothetical immunity region protein 8 - Bacillus phage phi-105
C, Species: Bacillus phage phi-105
A;Note: host Bacillus subtilis
C;Date: 20-Aug-1999 #sequence revision 20-Aug-1999 #text change 20-Aug-1999
C;Accession: G24521
R;Cully, D.F.; Garro, A.J.
Gene 38, 153-164, 1985
A; Title: Nucleotide sequence of the immunity region of Bacillus subtilis bacteriophage p
A; Reference number: A91535; MUID:86056972; PMID:3934047
A; Accession: G24521
A; Molecule type: DNA
A;Residues: 1-44 <cul></cul>
A; Cross-references: GB:M11920; NID:q215477
C; Comment: This is the hypothetical translation of a sequence that was not reported as a
Chigary Match EA 09. Conta 30. DB 4. Langth 44.

# ö 1; Indels

Gaps rengtn 44; 50.0%; Score 29; DB 66.7%; Pred. No. 71; cive 2; Mismatches Query Match Best Local Similarity 66.7 Matches 6; Conservative σ 1 RIALRYRIL ò

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C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000 C;Accession: B82581 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 below hypothetical protein XF2242 [imported] - Xylella fastidiosa (strain 9a5c)

A;Status: preliminary A;Molecule type: DNA

A; Residues: 1-54 <SIM>

A; Cross-references: GB:AE004037; GB:AE003849; NID:g9107394; PIDN:AAF85041.1; GSPDB:GN001 A; Experimental source: strain 9a5c
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; P. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer.; as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Franca, S.C.; Franco, M.C.; Frob., J.D.; Junqueira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.B.; Laigr, Ando, M.A.; Madeira, A.M.B.N; Madeira, H.M.F.; Martuns, E.M.; Martuns, E.M.; Mayaki, C.Y., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P.

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C;Accession: C97788
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
Science 293, 2093-2098 (2001)
A;Title: Mechanisms of Evolution in Rickettsia conoril and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir: Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B83853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-58 <KUR>
A;Cross-references: GB:AE006914;
                                                                                                                                                                                                                                                                                      hypothetical protein RC0707 [imported] - Rickettsia conorii (strain Malish C;Species: Rickettsia conorii C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001 C;Accession: C97788
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A;Authors: da Silva, A.C.R.;
M.; Tsuhako, M.H.; Vallada, F
A;Reference number: A59328
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C;Date: 01-Dec-2000 #sequence_revision
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da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
                                                                                                                                                   PIDN: AAL03245.1;
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RESULT

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C;Species: Streptococcus phage phi-O1205
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 24-Sep-1999
C;Accession: T13307
R;Stanley, E; Fitzgerald, G.F.; Le Marrec, C.; Fayard, B.; van Sinderen, D.
Microbiology 143, 3417-3429, 1997
Microbiology 143, 3417-3429, 1997
A;Title: Sequence analysis and characterization of phi O1205, a temperate bacteriophage A;Reference number: Z17554; MUID:98048466; PMID:9387220
A;Accession: T13307
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                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-52 <KUR>
                                                                                                                                                                                                                                                                                                 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, .; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
                                                                                                                                                                                                                                                                                                                                                                       C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: F96947
                                                                                                                 A; Cross references: GB: AB001437; PIDN: AAK78369.1; A; Experimental source: Clostridium acetobutylicum
                                                                                                                                                                                                                             A; Title: Genome Sequence and Comparative Analysis of the A; Reference number: A96900; MUID:21359325; PMID:21359325 A; Accession: F96947
                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein CAC0389 [imported] - Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U88974; NID:g2444080; PID:g2444098; PIDN:AAC79534.1
A;Experimental source: host Streptococcus thermophilus strain CNRZ1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-50 < STA>
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(;Species: Streptococcus phage phi-O1205
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 24-Sep-1999
C;Accession: T13307
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Query Match
Best Local Similarity
                                                                                              Genetics:
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Pred. No. 1.56
4; Mismatches
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Pred. No.
    Score 27;
Pred. No.
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hypothetical protein 45 - Escherichia coli cryptic lambdoid prophage DLP12 (5) Escherichia coli (5) Escherichia (5) E
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C;Species: chloroplast Chlorella vulgaris
C;Species: chloroplast Chlorella vulgaris
C;Species: chloroplast Chlorella vulgaris
C;Species: chloroplast Chloroplast
C;Accession: T07202
E;Makasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Nakasugi, T.; Nagai, T.; Nakai, Nagai, T.; Nagai, T.
                                           A;Cross-references: EMBL:X92587; NID:g1051136; PIDN:CAA63322.1; PID:g1051142 C;Genetics:
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43.1%; Score 25; DB 1; Length 46;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels
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C;Superfamily: phage 82 hypothetical protein 45
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C; Keywords: chloroplast
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A, Molecule type: DNA
A, Residues: 1-46 < MAH>
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C; Species: Neisseria meningitidis
C; Species: 13.4mz-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C; Accession: B81006
R; Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Um, H.; Vanathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A; Authbors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A; Accession: B81006
A; Accession: B81006
A; Accession: B81006
A; Reterence number: A81000; MUID:20175755; PMID:10710307
A; Residues: 1-29 cTET-
A; Cross-references: GB:AE002559; GB:AE002098; NID:97227357; PIDN:AAF42414.1; PID:9722736
A; Experimental source: serogroup B, strain MC58
C; Genetics:
A; Genetics:
A; Genetics:
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C;Species: Thermus agnaticus
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C;Accession: C48401
B;Accession: C48401
B;Chimie 74, 327-336, 1992
B;Chimie 74, 327-336, 19
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: S65884
R;Mahdi, A.A.; Sharples, G.J.; Mandal, T.N.; Lloyd, R.G.
J. Mol. Biol. 257, 561-573, 1996
A;Title: Holliday junction resolvases encoded by homologous rusA genes in Escherichia cc
A;Title: Holliday junction resolvases encoded by homologous rusA genes in Escherichia cc
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                                                        4; Indels
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                                                  1; Mismatches
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                                           Conservative
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19 RFSLLLRF 26
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hypothetical protein 51 - Plasmodium falciparum plastid
C;Species: plastid Plasmodium falciparum
C;Species: plastid Plasmodium falciparum
C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 08-Oct-1999
C;Accession: S72280
R;Wilson, R.J.M.; Denny, P.W.; Preiser, P.R.; Rangachari, K.; Roberts, K.; Roy, A.; Whyt
J. Mol. Biol. 261, 155-172, 1996
A;Title: Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium fa
A;Reference number: S72277; MUID:96346169; PMID:8757284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Ju1-2000
C;Accession: C72257
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                             Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sec
A:Reference number: A72200; MUID:99287316; PMID:10360571
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A;Accession: A04429
A;Molernia
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C;Species: phage T7
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 23-Jul-1999
C;Accession: A04429; S42341
R;Dunn, J.J.; Thompson, K.
submitted to the Nucleic Acid Sequence Database, September 1982
                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-50 <ARNs
A;Residues: 1-50 <ARNs
A;Cross-references: GB:AE001793; GB:AE000512; NID:g4981963; PIDN:AAD36473.1;
A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: A72200;
A;Accession: C72257
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C; Superfamily: phage T7 gen
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J. Mol. Biol. 166, 477-535, 1983
A;Title: Complete nucleotide sequence of bacteriophage T7
A;Reference number: S42283; MUID:83241725; PMID:6864790
A;Accession: S42341
A; Accession:
                                                                                                                                                                                                                                RESULT 15
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A; Residues: 1-49 <DUW>
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A; Residues: 1-49 < DUN >
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Gene: TM1402
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4.8e+02;
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on, D.;
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A; Genome: plastid A_i; Note: this apparently degenerate plastid is referred to as the apicoplast C_i; Keywords: plastid
                                                                                                                                                                                                                A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Mossidues: 1-51 - WIL-
A;Cross-references: EMBL:X95275; NID:g1171583; PIDN:CAA64570.1; PID:e220241; PID:g117158
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996
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                                                                     Query Match
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Matches 4; Conserv
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Pred. No. 4.9e+02;
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Search completed: December 19, 2002, 16:22:59 Job time: 11.4118 secs

PYY analogue, SEQ Human protective D Propionibacterium

Perfect score:

Run on:

Scoring table: Sequence:

Searched:

Database

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AAY87564
AAU73323
AAU53267
       23
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| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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                             GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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58
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description -	Fragment of human	Propionibacterium	Immunosuppressive	Human Class I HLA-	HLA-B2702 CTL modu	Immunomodulating d	Human immune/haema			
SUMMARIES			ΙD	AAY76338	AAU59703	AAY72482	AAB59457	AAB59416	AAB59417	AAB59418	AAR92911	AAW33779	AAM83083
			DB	21	22	22	22	22	22	22	16	19	22
			re Match Length DB I	38	57	10	10	14	14	14	20	20	46
	de	Query	Match	67.2	67.2	62.1	62.1	62.1	62.1	62.1	59.5	59.5	56.9
			Score	39	39	36	36	. 36	36	36	34.5	34.5	33
		Result	No.		7	m	4	ß	9	7	80	6	10

Fundan Class I HIA- Protegrin derivati Phosphatidylserine Novel human diagno Peptide #3746 enco Peptide #3796 enco Human brain expres Human brain expres Human bone marrow Peptide #3720 enco Peptide #3720 enco Peptide #3823 enco Peptide #3825 enco Miniature protein Human ovary specif Synthetic fragment Human cvary specif Synthetic fragment		AAY76338 standard; Protein; 38 AA.  AAY76338; 23-MAR-2000 (first entry) Fragment of human secreted protein encoded by gene 38.  Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; achizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; therapy.  Homo sapiens.  WO9958660-A1.  18-NOV-1999; 99WG-0085094.  12-MAY-1998; 99WG-0085094.  12-MAY-1998; 99WG-0085094.  12-MAY-1998; 99WG-0085096.  18-MAY-1998; 99WG-0085006.  18-MAY-1998; 99WG-0085920.
AANS9419 AAW99406 AAW99406 AAB31095 ABB31095 ABB31654 AAM57061 AAM17286 AAM17286 AAM17286 AAM17808 AAM17808 AAM17808 AAM17808 AAM17808 AAM17808	ABB78836 AAR58902 AAR8902 AAR5902 AAB714039 AAB142813 AAG1639 AAG3780 AAW33781 AAW47261 AAW47261 AAW47261 AAW47261 AAW47261 AAW47261 AAW47261 AAW47261 AAW47261	38 AA.  protein encc ncer; imm ' Alzheimer 'sthma; psor cardiovascu' ne disorder
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1111112222222 1411111222222222222222222		RESULT 1 AAY76338 1D AAY76 XX XX XX XX XX XX DE Fragn XX BE Fragn XX BE Charter XW SChiz XW Schiz XW Autol XW Atler XW Autol XX XX Autol XW Autol XX Autol X

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18-MAY-1998;
18-MAY-1998;
                                                                                                                                                SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders -
                   01-NOV-2001
                                                        WO200181581-A2
                                                                                            Propionibacterium acnes
                                                                                                                                 dermatological; osteopathic; neuroprotectant
                                                                                                                                                                                                                        Propionibacterium acnes immunogenic protein #20599
                                                                                                                                                                                                                                                               27-FEB-2002
                                                                                                                                                                                                                                                                                                                                      AAU59703 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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18-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ALRYYRLAIR 12
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AIRYYREAVR 18
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w. Endress (
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98US-0085924.
98US-0085928.
98US-0085925.
98US-0085927.
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ing PE, Wei E
3A, Ebner R;
                                                                                                                                                                                                                                                                                                                                        57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB Pred. No. 2.5; 2; Mismatches
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Vei F, Brewer LA,
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RESULT 3
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Matches
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02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the prin specification, but was obtained in electronic format directly from WI at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention
                                                                         Immunosuppressive; allograft rejection; topological parameter; physico-chemical parameter; in silico screening; pharmaceutical; cosmetic; agrochemical; biomaterial; veterinary application.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                      Unidentified
                                                                       cosmetic; agrochemical; biomaterial;
                                                                                                                                                      Immunosuppressive peptide, P15, to prevent allograft rejection
                                                                                                                                                                                             24-APR-2001
                                                                                                                                                                                                                                                                         AAY72482 standard; peptide; 10 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful i
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WO200079263-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 7; Conserv
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; 2000US-216747P.
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ve J, Zhang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 2
Pred. No. 3.9;
4; Mismatches
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15-MAY-2000; 2000WO-EP04338.

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1 RIALRYY
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                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                         The present invention relates to a method for identifying physico-chemical and/or topological parameters associated with biological activity. The method involves selecting the first subset from the method involves selecting the first subset from predetermined set of physico-chemical parameters, determining their value of function, and selecting the second subset from physico-chemical parameters based on the values of function, such that each second subset is more closely associated with the activity than the first subset. The selected physico-chemical parameters are useful for developing criteria is more closely associated with the activity than the first subset. The selected physico-chemical parameters are useful for developing criteria for screening of compounds. The compounds may be used in pharmaceuticals, cosmetics, agrochemicals, biomaterials and in veterinary applications. It is also useful as an antibiotic or antifungal agent. The present sequence is an immunosuppressive peptide, pls, identified by in silico screening. The immunosuppressive peptide, the peptide that prevents allograft rejection is tested in a heterotopic allograft model of mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                         Identifying active candidate molecules on the basis of selected physico-chemical parameters, for in silico screening of compounds useful in pharmaceuticals, cosmetics, veterinary applications and agrochemicals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; human leukocyte antigen-B; HLA-B; immunosuppressive;
cytotoxic T cell activation inhibition; cell transplantation;
natural killer cell activation inhibition; organ transplantation.
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                                                                                                                                                                                                                                                                                                                                                                                                                    62.1%; Score 36; DB 22; Length 10; 100.0%; Pred. No. 2.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                      Disclosure; Page 38; 55pp; English.
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            99EP-0401526
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Matches 7; Conservative
                                                          Lahana R, Clair P,
                                                                                  WPI; 2001-091623/10
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                                  (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                             10 AA;
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3 RIALRYY 9
          18-JUN-1999;
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The present sequence is a peptide which may be used in a method for inhibiting activation of cytotoxic T lymphocytes and/or natural killer cells. The method involves combining the cells with a compound comprising an oligopeptide of at least 6 anino acids comprising a contiguous sequence of a human leukocyte antigen (HLA)-B alphal domain including amino acids 84-86 are YYW. The method is useful for transplanting a donor mammalian organ or cells to a mammalian recipient. The organ or cells are combined with the compound prior to implanting in the mammalian recipient, or the compound may be administered to the mammalian recipient, or the compound from prior to implanting the donor organ or cells.
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Inhibiting activation of cytotoxic T lymphocytes and/or natural killer cells involves combining cells with compound comprising oligopeptide with contiguous sequence of human leukocyte antigen-B alphal domain
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Pred. No. 2.1;
0; Mismatches 0; Indels
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                                                                                                                                                               Claim 12; Column 38; 20pp; English
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100.0%; Pred
0; N
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                          Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                 inhibiting activation of cytotoxic T lymphocytes and/or natural killer cells. The method involves combining the cells with a compound comprising an oligopeptide of at least 6 amino acids comprising a contiguous sequence of a human leukocyte antigen (HLA)-B alphal domain including amino acids 84-86, where amino acids 84-86 are YYW. The method is useful for transplanting a donor mammalian organ or cells to a mammalian recipient. The organ or cells are combined with the compound prior to implanting in the mammalian recipient, or the compound may be administered to the mammalian recipient in a period extending from prior to implanting the donor organ or cells.
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                                                                                      Sequence
                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                               Inhibiting activation of cytotoxic T lymphocytes and/or natural killer cells involves combining cells with compound comprising oligopeptide with contiguous sequence of human leukocyte antigen-B alphal domain -
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-111720/12.
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 1 RIALRYY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 RIALRYY 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RIALRYY 7
                                                                                                                                                                                                                                                                      present sequence is a peptide which may be used in a method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
7; Conserv
                                                                                      14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 AA;
                                                                                                                                                                                                                                                                                                  Column 7-8; 20pp; English.
                           62.1%; Score 36; DB ilarity 100.0%; Pred. No. 3. Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0433613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-0433613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.1%; Score 36; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                            DB 22;
3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organ transplantation
                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                          Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #17.
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                               0,
                                                                                                                                                                                                                                                        for
killer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                               0,
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RESULT 7
AAB59418
                                                                                  RESULT 8
AAR92911
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BXAXAXB
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                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                       cells. The method involves combining the cells with a compound comprising an oligopeptide of at least 6 amino acids comprising a contiguous sequence of a human leukocyte antigen (HIA)-B alphal domain including amino acids 84-86, where amino acids 84-86 are YYW.

The method is useful for transplanting a donor mammalian organ or cells to a mammalian recipient. The organ or cells are combined with the compound prior to implanting in the mammalian recipient, or the compound may be administered to the mammalian recipient in a period extending from prior to implanting the donor organ or cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytotoxic T cell natural killer ce
                       16-MAY-1996
                                               AAR92911;
                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting activation of cytotoxic T lymphocytes and/or natural killer cells involves combining cells with compound comprising oligopeptide with contiguous sequence of human leukocyte antigen-B alphal domain -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-111720/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Buelow R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6162434-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; human leukocyte antigen-B; HLA-B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB59418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB59418 standard; Peptide; 14
                                                                      AAR92911 standard;
                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a peptide which may be used in a method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SANG-) SANGSTAT MEDICAL CORP
                                                                                                                                                                                                                                                                                                                                                                      nhibiting activation of cytotoxic T
                                                                                                                                                                                              Local
                                                                                                                                                   1 RIALRYY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                   9
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7 RIALRYY 13
                                                                                                                                   RIALRYY 12
                                                                                                                                                                                  Similarity 7; Conserv
                                                                                                                                                                                                                                    14
                                                                                                                                                                                                                                                                                                                                                                                                          Column 7-8; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I HLA-B
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry
                       (first entry)
                                                                                                                                                                                                                                    AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0433613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0433613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activation
                                                                      peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alpha1-domain-derived peptide
                                                                                                                                                                                               62.1%; Score 36;
100.0%; Pred. No.
                                                                       20
                                                                                                                                                                                   <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                       lymphocytes and/or natural
                                                                                                                                                                                              3.1;
                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; immunosuppressive;
cell transplantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organ
                                                                                                                                                                                   ,.
                                                                                                                                                                                                          Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transplantation.
                                                                                                                                                                                   Indels
                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                       l for
killer
                                                                                                                                                                                  Gaps
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HLA-B2702 CTL modulating peptide

(B2702.84-75/84-75).

12, 18 ...

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24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM83083;
                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM83083
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                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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                                                                                                                                                                                                                                                                          AAR83061-R83085, AAR83090-R83096 and AAR92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched domor. The peptides are administered to a patient in conjunction with a subthersapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLS)
        Cytotoxic T lymphocyte, CTL, major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                 Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34.5; DB 16;
Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                          Parham P
                                                                                                                                                    (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                          Example 15; Page 36; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW33779 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunomodulating dimer peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                       59.5%;
                                                                                                             95WO-US04349
                                                                                                                                  94US-0222851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-US08689
                                                                                                                                                                         Krensky AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RIALRY---YRLAIR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RLAIRLNERYRLAIR 16
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                     20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunomodulating
                                                                                                                                                                                                                                                                                                                                                                                  of the patient.
                                                                                                                                                                         Clayberger C,
                                                                    WO9526979-A1
                                                                                                           05-APR-1995;
                                                                                                                                 05-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9744351-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAY-1997;
                                                                                       12-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-NOV-1997
                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW33779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW33779
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This sequence represents a specifically claimed immunomodulating dimer peptide of the invention. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal caylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-771) (aa79-64) or (aa84-79) (laa77-768); aa76 = B or V, aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or small amino acid, aa82 = R or L; aa83 = G or R; and as represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the profiferation of reals in response to anti-CD3. The peptide can be used for preventing rejection of transplants and lupus erythematosis. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                        New immunomodulating dimer peptide(s) - based on a Class I HLA-I alpha-1 domain, used for preventing rejection of transplants or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 19; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune/haematopoietic antigen SEQ ID NO:10676.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34.5; DB Pred. No. 8.7; 2; Mismatches
                                                                                                                                                                    Krensky AM;
                                                                               (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM83083 standard; Protein; 46 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 16; Page 35; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                            treating autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 2000US-0180628.
; 2000US-018464.
; 2000US-0186350.
; 2000US-018974.
; 2000US-0198123.
96US-0653294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0179065
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                                                                                                                                                                    Clayberger C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:|:|
2 RLAIRLNERYRLAIR
                                                                                                                                                                                                                                                    WPI; 1998-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAR-2000;
18-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAR-2000;
16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-2001
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                                                                                                                                                                    Beulow R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE SECTION OF THE SE
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19-MAY-2000; 07-JUN-2000; 28-JUN-2000; 30-JUN-2000; 07-JUL-2000; 07-JUL-2000;

> S-0205515. S-0209467. S-0214886. S-0215135. S-0216647.

11-JUL-2000; 11-JUL-2000; 14-JUL-2000; 26-JUL-2000;

2000US 2000US

-0217487.

-0216880

-0218290

14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000;

2000US

-0224518 -0224519

2000US-022567.
2000US-022568.
2000US-022570.
2000US-0225755.
2000US-0225759.
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2000US-0226681.
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2000US-0226681.
2000US-0226681.
2000US-0227182.
2000US-0227182.
2000US-0229287.
2000US-0229343.
2000US-0229343.
2000US-0229343.
2000US-0229343.
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17-NOV-2000
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06-DEC-2000
08-DEC-2000
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20-OCT 2000

20-OCT 2000

20-OCT 2000

20-OCT 2000

20-OCT 2000

01-NOV 2000

08-NOV 2000

01-NOV 2000

01-NO
                                                                                                                Nucleic acids encoding useful for preventing, metastasis -
                                                                                                                                                                                            WPI; 200
N-PSDB;
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I)
                                                                             Claim 11; SEQ
                                                                                                                                                                                                                                                      Rosen
                                                                                                                                                                                                                                                                                           (HUMA-)
                                                                                                                                                                                              2001-483426/52.
DB; AAK55864.
                                                                                                                                                                                                                                                    CA,
                                                                                                                                                                                                                                                                                           HUMAN
                                                                                                                                                                                                                                                    Barash SC,
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2000US-0254097.
2001US-0259678.
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2000US-0251988
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2000US-025179
2000US-0251479
2000US-0251856
2000US-0251868
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2000US-0249215.
2000US-0249216.
2000US-0249217.
2000US-0249214.
2000US-0249244.
2000US-0249244.
2000US-0249264.
2000US-0249264.
2000US-0249265.
2000US-0249299.
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2000US-0249207.

2000US-0249208.

2000US-0249209.

2000US-0249210.

2000US-0249211.

2000US-0249211.

2000US-0249213.
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2000US-0246528.
2000US-0246532.
2000US-0246532.
2000US-0246610.
2000US-0246611.
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2000US-0246523.
2000US-0246524.
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2000US-0241786.
2000US-0241787.
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2000US-0250160.
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2000US-0241809
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                                                                           NO 10676; 3071pp +
                                                                                                                                                                                                                                                                                           SCI INC
                                                                                                                                   human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and
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                                                                                                                                                                                                                                                      SM.
                                                                           Sequence Listing; English.
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14-AUG-2000
14-AUG-2000
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18-AUG-2000
22-AUG-2000
22-AUG-2000
23-AUG-2000
23-AUG-2000
20-SEP-2000
01-SEP-2000
01-SEP

3-0232400 3-0232401 3-0231413. 3-0231414. 3-0232080.

2000US. 2000US

3-0235834. 3-0235836. 3-0236327.

-0235484

1-0236367. 1-0236368. 1-0236369. 1-0236370.

3-0236802. 3-0237037. 3-0237038. 3-0237039. 3-0237040. 3-0239935. 3-0239937.

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proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting protein. (I) proteins and polynucleotides may be used to prevent and culturing the cell to express the diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK5492 to AAK54950 and AAM8169 represent sequences used in the exemplification of the present invention.
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54.5%;
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Query Match
Best Local Similarity 54.5
Matches 6; Conservative

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Gaps

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DB 22; Length 46; 41; 3; Indels

Score 33; DB 2 Pred. No. 41; 2; Mismatches

4 IVLIYYKLGVR 14 2 IALRYYRLAIR 12 ò 셤

AAY87564 standard; peptide; 10 AA. 18-JUL-2000 AAY87564; RESULT 11 AAY87564 

PYY analogue, SEQ ID NO:16 (first entry)

PYY analogue, peptide YY, electrolyte secretion, fluid secretion, nutrient uptake, lipolysis, vasoconstriction; gastrointestinal disorder, diarrhoea, Crohn's disease, irritable bowel syndrome, ileostomy, cachexia

Synthetic

Location/Qualifiers Key Modified-site

10 /note= "C-terminus is esterified to a methyl group"

US6046167-A.

04-APR-2000

98US-0047986. 25-MAR-1998;

98US-0047986. 25-MAR-1998;

(UYCI-) UNIV CINCINNATI

WPI; 2000-327889/28. Balasubramaniam A;

New peptide YY analogs especially useful for treating gastrointestinal disorders associated with excess intestinal electrolytes and water secretion, and decreased absorption, e.g. infectious and inflammatory diarrhea

Claim 24; Column 5; 18pp; English.

Sequences AAY87551-Y87564 and AAY87568 represent novel analogues of peptide YY (PYY) that can be used for the treatment of gastrointestinal disorders. PY (AAY87549, AAY87550) is a 36 residue peptide amide that is released into the circulation after a meal and which is thought to play a role in regulating intestinal secretion and absorption. It binds

to a receptor on intestinal epithelial cells, and inhibits intestinal secretion and gut motility. It is therefore a natural inhibitor of diarrhoea. Pry has also been implicated in nutrient uptake, cell corporation. Iipolysis and vasoconstriction. The compounds of the invention are useful for inhibiting fluid and electrolyte secretion in the sugmenting nutrient transport; increasing cell corporates are useful for inhibiting fluid and electrolyte secretion in the gastrointestinal tract; regulating injolysis in, corporated with excess intestinal blood flow in mammals. The analogues are especially useful in the treatment of gastrointestinal disorders associated with excess intestinal electrolytes and water corporated with excess intestinal electrolytes and water secretion, as well as decreased absorption. For example, they are useful in treating acute viral or bacterial diarrhoea, diarrhoea due to protozoal infections, travellers' diarrhoea, diarrhoea due to protozoal infections, travellers' diarrhoea; inflammatory diarrhoea (e.g., Crohn's disease, irritable bowel syndrome); short bowel syndrome; or diarrhoea following ileostomy. The peptides can also be used to treat diseased. A service of the pry analogues are shorter than naturally occurring PPY, synthesis and purification of the compounds is easier and less costly. The analogues interact specifically with PTY receptors and not with receptors for the pry homologue neuropeptide Y (NPY), thus minimising unwanted ö Gaps .; 0 DB 21; Length 10; 12; 0; Indels 55.2%; Scor. 100.0%; Pred. No. ... 6; Conservative Query Match Best Local Similarity 10 AA; side reactions. σ 4 LRYYRL Sequence Matches ð

œ 3 LRYYRL

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RESULT 12

AAU73323 standard; Peptide; 36 AA. AAU73323

12-MAR-2002 (first entry)

AAU73323;

Human protective DNA sequence CNI-00738 open reading frame #44.

ischaemia, open reading frame, ORF; cerebral herniation, septic embolism, cerebral oedema, meningitis, protozoal infection, malaria, CNI-00733; metazoal infection, vascular disease, eye, macular degeneration, trauma, diabetic retinopathy; epidural haematoma; tumour; degenerative disease, nutrittional condition; environmental condition; metabolic condition; CNI-00736; CNI-00738; CNI-00742; CNI-00748; cancer; gene therapy. Human; protective sequence; cell death; central nervous system; stroke; THE STATE OF THE S

Homo sapiens.

WO200181361-A1.

01-NOV-2001.

09-APR-2001; 2001WO-US11501.

11-APR-2000; 2000US-0547938.

(COGE-) COGENT NEUROSCIENCE INC.

Thomas MB; Barney S, Lo DC, Katz LC, Portbury SD, Puranam K,

WPI; 2002-066433/09. N-PSDB; AAS98485.

Polypeptides and polynucleotides comprising protective sequences useful for preventing, delaying or rescuing a cell from death in disease, condition or disorders such as Alzheimer's disease, stroke, tumours,

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RESULT 13
AAU53267
ID AAU53
XX AAU53
XX AAU53
XX SAPHO
KW LIVELT
KW LINFLA
KW LINFLA
KW LOPIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; EIISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                            Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful :
                                                                                                                                                                                                                                                L'maisonneuve
                                                                                                                                                                                                                                                                                                                                                                                                21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU53267 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Fig 6AU; 228pp; English
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                                      vulgaris
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, Jen S, Carter I
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central
                                                                           Inhibiting activation of cytotoxic T lymphocytes and/or natural killer cells involves combining cells with compound comprising oligopeptide with contiguous sequence of human leukocyte antigen-B alphal domain -
                                                                                                                                                                                                                                                                                                                                                                                                                               Human; human leukocyte antigen-B; HLA-B; immunosuppressive; cytotoxic T cell activation inhibition; cell transplantation; natural killer cell activation inhibition; organ transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                               WPI; 2001-111720/12.
                                                                                                                                                                                                                                               03-MAY-1995;
                                                                                                                                                                                                                                                                              03-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Class I HLA-B alphal-domain-derived peptide #19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAR-2001
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Pred. No. 79;
3; Mismatches
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                                            English
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The present sequence is a peptide which may be used in a method inhibiting activation of cytotoxic T lymphocytes and/or natural

tor killer

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cells. The method involves combining the cells with a compound comprising an oligopeptide of at least 6 amino acids comprising a contiguous sequence of a human leukcyte antigen (HLA) Balphal domain including amino acids 84-86, where amino acids 84-86 are YYW. The method is useful for transplanting a donor mammalian organ or cells to a mammalian recipient. The organ or cells are compined with the compound prior to implanting in the mammalian recipient, or the compound may be administered to the mammalian recipient in a period extending from prior to implanting the donor organ or cells.
                                                                                                                                                                                                                                                                                                                                                                                                               53.4%; Score 31; DB 22; Length 13; 100.0%; Pred. No. 24; cive 0; Mismatches 0; Indels
Thu Dec 19 16:37:42 2002
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
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Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier Protegrin derivative peptide SM2187. AAW99406 standard; peptide; 18 AA. (first entry) 08-JUN-1999 AAW99406; RESULT 15 AAW99406

Kaczorek M; Grassy G, 98WO-FR01757, 97FR-0010297. Chavanieu A, WPI; 1999-190034/16. (SYNT-) SYNT:EM SA. 06-AUG-1998; 12-AUG-1997; WO9907728-A2 18-FEB-1999 Synthetic. Calas B, 

This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The newel derivatives are linear and lack the genet to an organism, e.g. therapeutic proteins, antibodies for their fragments), nucleic acid, oligonucledtides, ribozymes, antitumour agents antivirals and anti-inflammatories, etc. The derivatives are non-toxic mechanism, so can deliver active agents to cytoplasm and non-live active agents including crossing the blood-brain barrier. Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells Claim 7; Page 28; 37pp; French.

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18 AA; Sequence

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Score 31; DB 20; Length 18; Pred. No. 35;
  53.4%;
58.3%;
Query Match
Best Local Similarity
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Matc	hes	7;	Matches 7; Conservative	1;	1; Mismatches 4; Indels	4,	Indels	0;	0; Gaps
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Search completed: December 19, 2002, 16:19:07 Job time : 29.5882 secs

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December 19, 2002, 16:14:32; Search time 21.1765 Seconds (without alignments) 116.760 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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sp\_archerap:\* 112: 113: 114: 116:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Q8xft3 salmonella 027979 archaeoglob 028493 mirounga le Q9u982 trichinella Q92h13 homo sapien Q951r3 anthomurice Q8xv69 pyrobaculum Q8t946 drosophila Q959fb rickettsia Q958t8 colocasia Q65737 bluetongue Q95737 bluetongue Q9pc59 xylella fas Q9nle7 leishmania Q8v7e7 tt virus. Description QBXFT3 Q27979 Q2493 Q9U9S2 Q9C1B3 Q9S1R3 Q9S1R3 Q9S1R3 Q9S1R3 Q9S77 Q9S737 Q9C5737 Q9C5737 Q9C5737 Q9C757 Q 16 B Query Match Length Score 228 228 228 228 228 228 228 238 Result No. 

O95596 homo sapien	Q05167 saccharomyc	Q9tww4 lymnaea sta	P75718 escherichia	044363 ceratitis c	Q98e76 rhizobium l	Q50087 mycobacteri	O90630 baboon herp	O90633 baboon herp	Q95he9 papio anubi	Q95he8 papio anubi	papio			Q95he4 papio anubi		Q95hel papio anubi	Q95he0 papio anubi		papio	papic	O19688 homo sapien	P78340 homo sapien			Q9sk54 arabidopsis		Univ naimia 09w8y9	Q9w132 drosophila
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Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Pleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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Q28493;
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NCBI_TaxID=9715;
                        Eukaryota; Metazoa; Chordata; (Mammalia; Eutheria; Carnivora;
                                                                    Mirounga leonina (Southern elephant seal).
                                                                                              Histone H2AF (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Complete proteome. SEQUENCE 56 AA; 6986 MW; DBDA220C268A7DF6 CRC64;
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MEDLINE=98049343; PubMed=9389475;
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Archaea; Euryarchaeota; Archaeoglobi;
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Nature 413:848-852(2001)
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reducing archaeon Archaeoglobus fulgidus.";
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protein AF2305.
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ia; Phocidae; Mirounga.
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Q92HL9;
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MEDLINE=21442074; PubMed=11557893; Ogata H., Audic S., Renesto-Audiff
                                                                                                                                     Rickettsia conorii.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
Hypothetical protein RC0752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Semyenova S.K., Chrisanfova G.G.; "RAPD-derived Trichinella pseudospiralis probe."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ dat EMBL; AF153496; AAD45671.1; -.
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01-MAY-2000
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                                                                                                           NCBI_TaxID=781;
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MEDLINE=94214718; PubMed=7909260;
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Pfam; PF00125; histone; 1.
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ilarity 54.5%;
Conservative
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    Renesto-Audiffren P.,
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58.3%;
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Pred. No.
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Drosopija melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bbhydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.,
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY070857, AAL48479.1; -.
SEQUENCE 56 AA, 6512 MW; E9803230DB63B169 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.";
Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
EMBL; AE009975; AAL64187.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 53 AA; 6120 MW; 73023B57A6AE8E7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 29; DB 17; Length 53; Pred. No. 3.3e+02;
                                                    Score 29; DB 8; Length 35;
Pred. No. 2.2e+02;
3; Mismatches 2; Indels
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 35 35
35 AA, 4214 MW, F41BC3BDE6F9B215 CRC64;
                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein PAE2427.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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54.5%; Pred. No. 3.-.
3; Mismatches
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STRAIN=IM2 / ATCC 51768 / DSM 7523;
PubMed=11792869;
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Thermoproteaceae; Pyrobaculum.
                                                      50.0%;
                                                                        Best Local Similarity 50.0
Matches 5; Conservative
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Best Local Similarity
Matches 6; Conserv
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SEQUENCE
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Q8T946;
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Q8ZV69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     France S.C., Hoover L.L.;
"Analysis of variation in mitochondrial DNA sequences (ND3, ND4L, MSH)
among Octocorallia (Chidaria: Anthozoa).";
Proc. Biol. Soc. Wash. 0:0-0(2001).
EMBL; AF385304; AAK68137.1; -.
Mitochondrion.
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             Racult D.;
"Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
Science 293-2098(2001).
BEMBL, AR008632; AAL03290.1; -
InterPro, IPR001440; TPR.
Hypochetical protein; Complete proteome.
SEQUENCE 52 AA; 6293 MW; 5A2C8F20C839BD36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo Sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Cnidaria; Anthozoa; Alcyonaria; Gorgonacea;
Holaxonia; Plexauridae; Anthomuricea.
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
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                                                                                                                                                                51.7%; Score 30; DB 16; Length 52; 50.0%; Pred. No. 2.1e+02; Live 3; Mismatches 2; Indels
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last annotation update)
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Q9P138;
Q1-OCT-2000 (TEMBLE1. 15, C1
Q1-OCT-2000 (TEMBLE1. 15, L6
Q1-OCT-2000 (TEMBLE1. 15, L6
PRO2964:
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Matches 5; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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11 LAIKYYNSAI 20
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TISSUE=LIVER;
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Q9S8T8;
01-MAY-2000
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Q92JP5;
01-DEC-2001
                                                                                                                                                        Pfam; PFC
SEQUENCE
                                                                                                                                                                                   development.";
Plant Cell 4:1549-1559(1992).
InterPro: IPR002160; Kunitz legume.
InterPro: Iranitz legume; 1.
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2001 (TrEMBLrel. 18,
Globulin G2B (Fragment).
                                                                                                                                                                                                                                                                                         SEQUENCE.

MEDLINE=93104679; PubMed=1467653;

de Castro L.A., Carneiro M., Neshich D de C.,

de Castro L.A. Carneiro M., Neshich D de C.,
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EMBL; AE008571; AAL02560.1; -.
InterPro; IPR001440; TPR.
SMART; SM00028; TPR; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 60 AA; 7160 MW; 4B5F2B0B5FB7021C CRC64;
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Ogata H., Audic S., Renesto-Audiffren P., Fo
Samson D., Roux V., Cossart P., Weissenbach
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colocasia esculenta (Elephant's ear) (Taro).
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STRAIN=MALISH
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                                                                                                                                                                                                                                                                                    'Spatial and temporal gene expression patterns
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NCE 25 AA;
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3; Mismatches 1;
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                                                                                 2.4e+02;
                                                                                                         DB 10;
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th J., Claverie J.-M.,
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RA Alvarenga R., Alves L.M.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S. RA Colauto N.B., Camargo A.A., Camargo L.B.A., Carraro D.M., Carrer H., RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Racincani A.D., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Racincani A.D., Franca S.C., Franco M.C., Frohme M., Furlan L.R., RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., RA Garnier M., Goldman G.H., Gomes S.L., Gruber A., RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., RA Garnier M.D., Junqueira M.L., Kemper B.L., Kitajima J.P., RA Hop L., Hoheisel J.D., Junqueira M.L., Kemper B.L., Kitajima J.P., RA Garnier B.C., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., RA Lemos B.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L., Martins E.M.F., Marino C.L., Marchado M.A., Marcins B.A.L., Martins E.M.F., Matsukuma A.Y., RA Monn D.H., Nagai M.A., Nascimento A.I.T.O., Netto L.E.S., Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., RA Monn D.H., Nagai M.A., Nascimento A.I.T.O., Netto L.B.S., RA Monn D.H., Nagai M.A., C., Palmieri D.A., Paris A., RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
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Best Local S
Matches 6
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Q65737;
01-NOV-1996
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2002 (TrEMBLrel. 20,
Hypothetical protein Xf1922.
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[1]
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Viruses; dsRNA vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20365717; PubMed=10910347;
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Last annotation updat
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Pred. No. 3.4e+02;
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Arch. Virol. 147:21-41(2002).
BABBL; AB064612; BAB79368.1; -...
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=FRIEDLIN;
Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL160493; CAB98113.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                 LMŽ6.495.
Leishhmania major.
Eukaryota: Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr., da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., Vallada H., Van Silvs M.A., Verjovski-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meidanis J., Setubal J.C., "The genome sequence of the plant pathogen Xylella fastidiosa.", marure 406:151-159(2000)

BNBL, ABONGOLIZ, AAF84728.1; --
Hypothetical protein; Complete proteome.

SEQUENCE 40 AA; 4533 MW; 96296103833C1B08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=21844401; PubMed=11855633;
Peng Y.H., Nishizawa T., Takahashi M., Ishikawa T., Yoshikawa A.,
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                                                                                                                                                             Score 28; DB 16; Length 40;
Pred. No. 3.8e+02;
0; Mismatches 2; Indels
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Pred. No. 5.4e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 57 AA; 6498 MW; 6DF143AEF1C8C0D1 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Hypothetical 6.5 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
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TT virus.
Viruses; ssDNA viruses; unclassified ssDNA viruses.
NCBI_TaxID=68887;
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Q9NLE7
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SQ SEQUENCE 57 AA; 8138 MW; 61E467DDE395ACE9 CRC64;

Query Match 48.3%; Score 28; DB 12; Length 57;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps
Qy 5 RYYRLAIR 12

Db 48 RYYRRIR 55

Search completed: December 19, 2002, 16:21:53
Job time: 22.1765 secs
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December 19, 2002, 16:03:12 ; Search time 5.47059 Seconds (without alignments) 90.980 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                 OM protein - protein search, using sw model
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US-08-653-294C-40 58 1 RIALRYYRLAIR 12 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

5116 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 60

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	P10431 b		P82542 squalus aca		P81468 mesocricetu	O83305 treponema p	Q00932 yersinia ps	mycoplasm				O51309 borrelia bu		gallus			Q01434 bacteriopha	P00982 dendroaspis		O51646 borrelia bu	P80437 streptomyce		-	P80167 gadus morhu	P29071 oncorhynchu		oryct			P29205 amia calva	P09473 lepisosteus	09474	P29206 raja rhina
SUMMARIES		ΩI	M8 B	LPA2_BACSU	PLMS SQUAC	DEF2 MESAU	DEF4_MESAU	Y281 TREPA	LCRT YERPS	RS21_MYCPN	PSBY_PORPU	HSP1_HUMAN	HSP1_PONPY	Y331_BORBU	Y072 NPVOP	MGN_CHICK	PSAM CYAPA	PMY_PETMA	YOOD BPT4	IVBK DENAN	LHA1 RHOSH	RL32_BORBU	HPAA_STRGD	AMPM_BOMMO	PSAM_GUITH	NEUY_GADMO	NEUY ONCMY	NEUY_PIG		NEUY_RANRI	NEUY_SHEEP	PYY_AMICA		PYY_ONCKI	PYY_RAJRH
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RESULT 2

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36 1 PYY RANRI 37 1 SPYY PHYBI 37 1 PSYY CHICK 45 1 PYY CHICK 45 1 YSK6 SSV1 49 1 HSPI SAGIN 51 1 HSPI ALOSE 54 1 RX2 TOBAC 56 1 RX2 BACHD 57 1 IVBK DENPO 58 1 FER6 METJA 59 1 YASO_ARCFU	ALIGNMENTS 1D; PRT; 44 AA.	Created) Last sequence update) Last annotation update) region protein 8. ', no RNA stage; Caudovirales;	3934047; ne immunity region of Ba entification of the repr '';	ISS-PROT entry is copyright. It is produced the the Swiss Institute of Bioinformatics and topean Bioinformatics Institutions as long as its connon-profit institutions as long as its construction as a long as its construction as a long as its construction and this statement is not removed. Usage by requires a license agreement (See http://www.an email to license@isb-sib.ch).	NOTATED_CDS.  WW; C440D1B134841832 C	8%; Score 37; DB 1; .5%; Pred. No. 0.54; e 4; Mismatches 1
334 335 336 336 336 337 338 338 338 338 339 337 347 347 347 347 347 347 347 347 347	J. 1 BPPH1 YIM8_BPPH1 STANDARD;	(Rel. 10, 9 (Rel. 10, 9 (Rel. 10, al immunity age phi-105. sDNA viruses = Viruses.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=86056972; PubMed=3934047; Cully D.F., Garro A.J.; "Nucleotide sequence of the immunity bacteriophage phi 105: identification mRNA and protein products."; Gene 38:153-164(1985).	SWIS Burol by fied ties	1920; 521; ical	/ Match Local Similarity 5 local 6, Conservati 2 IALRYYRLAIR 12 3                   9 LLLRYFRLALK 19
	RESULT YIM8 BI ID Y	Artigo oo o	RR	388888888	SOWER	Query Best Match Qy Db

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RA Azevedo V. Bertero M.G., Bessieres P. Bolotin A.M., Alloni G.,
RA Azevedo V. Bertero M.G., Bessieres P. Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
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RA Choi S.K., Codani J.J., Lagaret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Haga K., Haiech J., Galizzi A., Galleron N.,
RA Glim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Misuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Noone D., O'Reilly M., Portetelle D., Porwollik S., Prescott A.M.,
RA Paresecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sato T., Scanlan S., Vandembol M., Vannier F., Vasaarotti A.,
RA Vasard A., Vannier E., Wedler E., Wedler H., Weitzenegger T.,
RA Vishida K., Vasamoto H., Vamane K., Yasamo
                              EMBL;
                                                                                                                                                   use by non-profit institutions as long as modified and this statement is not removed. Usentities requires a license agreement (See htt or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome subtilis.";
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                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There
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Chen N.-Y., Hu F.M.,
                                                                                          EMBL; J03294; AAA87317.1;
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FUNCTION: INVOLVED IN THE REPRESSION OF THE LYSC OPERON.
                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright.
een the Swiss Institute of Bio:
                          Z75208; CAA99579.1;
Z99118; CAB14808.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a H.F., Zumstein E., Yoshikawa H., Danchin A., sequence of the Gram-positive bacterium Bacillus
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J. Biol. Chem. 275:35969-35977(2000).
                                                                                                                                                                                                                                                           MEDLINE=21534268; PubMed=11676495; Schulurmans Stekhoven F.M.A.H., Flik G., Wendelaar Bong Schulurmans Stekhoven F.M.A.H.) and channels in rectal "N-terminal sequences of small ion channels in rectal sharks: a biochemical hallmark for classification and Biochem. Biophys. Res. Commun. 288:670-675(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phospholemman-like protein (PLMS) (Fragment).
Squalus acanthias (Spiny dogfish).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
Elasmobranchii, Squalea, Squaloidei, Squalidae, Squalus.
                                                                                                                     C (PK-C). Phosphorylated in response to stimulation (By similarity).

-i- SIMILARITY: BELONGS TO THE FXYD FAMILY. InterPro; IPR000272; ATP1G1 PLM MATB. PROSITE; PS01310; FXYD; FALSE NEG.

Transmembrane; Ionic channel; Ion transport
                                                                                       SEQUENCE
                                                                                                            Microsome.
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RFTYDYYRLRV
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                                                      Score 27;
Pred. No.
                                                                                       647BE1C060B2C9F1
                                                                                                                                                                                                                                                                                                                                                                  Cramb G.;
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A->G: ELEVATED LEVELS
H->L: ELEVATED LEVELS
5EA641D7B3FBC916 CRC64
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phylogeny?";
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PROSITE; PS00269; DEFI
Defensin; Antibiotic;
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17 VGLRCSRLSVR 27
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Best Local Similarity
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083305;
                                                                            DISULFID
DISULFID
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mak P., Wojcik K., Thogeren 1.B., Dubin A.;
"Isolation, antimicrobial activities, and primary structures of hamster neutrophil defensins."
"Isolation, antimicrobial activities, and primary structures of hamster neutrophil defensins."

"Infect. Immun. 64-4444-449(1996).
-!- FUNCTION: BACTERICIDAL ACTIVITY, GREATER AGAINST GRAM-POSITE BACTERIA. LOW ANTI-FUNGI ACTIVITY.
-!- SIMILARITY: BELONGS TO THE CORTICOSTATIN/DEFENSIN FAMILY.
-!- CAUTION: THE HANP-2 COULD BE A PRODUCT OF PROTEOLYTIC N-TERMINAL AMINO ACID REMOVAL FROM HANP-4.

InterPro: IPRO0123; defensin_mammal.
PF00123; defensin_mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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-!- FUNCTION: BACTERICIDAL ACTIVITY, GREATER AGAINST GRAM-POSITE
BACTERIA. LOW ANTI-FUNGI ACTIVITY.
-!- SIMILARITY: BELONGS TO THE CORTICOSTATIN/DEFENSIN FAMILY.
-!- CAUTION: THE HANP-2 COULD BE A PRODUCT OF PROTECLYTIC N-TERMINAL
AMINO ACID REMOVAL FROM HANP-4.
InterPro; IPRO0123; defensin mammal.
Fram; PRO0323; defensis. 1.
SMART; SM00048; DEFSN; 1.
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15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Neutrophil defensin 4 (HaMP-4).
Mesocricetus auratus (Golden hamster).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE.
MEDLINE=97045125; PubMed=8890190;
Mak P., Wojcik K., Thogersen I.B., Dubin A.;
"Isolation, antimicrobial activities, and primary structures of hamster neutrophil defension."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred. No. 54;
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                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
16-UNN-2014 (Gel. 41, Last annotation update)
Mesocricetus auratus (Golden hamster).
                                                                                                                           31 AA.
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                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00048; DEFSN; 1.
PROSITE; PS00269; DEFENSIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 AA; 3621 MW;
                                                                                                                   STANDARD;
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Best Local Similarity
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                                                                                                                   DEF2 MESAU
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DEF4_MESAU
                                                                                 DEF2_MESAU
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                                  RESULT 4
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                                                                                                                                                                         Length 33;
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23097FE7D474AD65 CRC64;
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NCBI_TaxID=160;
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SEQUENCE 42 AA; 4462 MW; P9FBAD73F78BCD7F CRC64;
                                                                                                                                                                         Score 26; DB 1;
Pred. No. 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein TP0281.
                                                                                                                                                                                                                          2; Mismatches
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DEFENSIN; 1.
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3821 MW;
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Science 281:375-388(1998)
                                                                                                                                                                                                                          5; Conservative
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LCRT_YERPS
ID LCRT YE
AC Q00932,
DT 01-JUL-
DT 01-JUL-
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Best Local
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P57079;
16-OCT-2001
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                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                 "Re-annotating the Mycoplasma pneumoniae genome value, function and reading frames."; Nucleic Acids Res. 28:3278-3288(2000).
                                                                                                                                                                                                                        Dandekar T., Huynen M., Regula J.T., Ueberle
Andrade M.A., Doerks T., Sanchez-Pulido L.,
Yuan Y.P., Herrmann R., Bork P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
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Yersinia pseudotuberculosis shows extensive
J. Bacteriol. 174:3355-3363(1992)
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                                                                                                                                                                                                                                                                                                                                                                                                     pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete sequence
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Himmelreich R., Hilbert H., Plagens H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2104;
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                            European Bioinformatics Institute.
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OR MPN296 OR MP539.1.
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Pred. No. 1.7e
1; Mismatches
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B., Suyama
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01-OCT-1996
15-DEC-1998
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SEQUENCE
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P51206;
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                                                                                                                        TRANSMEM
                                                                                                                                     Photosystem
DOMAIN
                                                                                                                                                              EMBL; U38804; AAC08092.1; -.

    -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane
    -!- SIMILARITY: BELONGS TO THE PSBY FAMILY.

    -!- FUNCTION: MANGANESE-BINDING POLYPEPTIDE
METABOLIZING ENZYME ACTIVITY. COMPONENT

                                                                                                                                                                                                                                                                                                                                               Plant Mol.
                                                                                                                                                                                                                                                                                                                                                             genome."
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Reith M.E., Munholland J.;
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II protein Y.
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AAG34754.1; -.
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50.0%;
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Pred. No. 1.8e+02
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STROMAL (POTENTIAL)
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RESULT 10 HSP1\_HUMAN ID HSP1\_HUMAN

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PIR, A26843; A26843.
PIR, A38515, A38515.
PIR, A33330; A3330.
PIR, A60896; A60896.
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                                                                                                                                                                                                                  Ammer H., Henschen A., Lee C.-H.;
"Isolation and amino-acid sequence analysis of human sperm protamines
Pl and P2. Occurrence of two forms of protamine P2.";
Biol. Chem. Hoppe-Seyler 367:515-522(1986).
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SEQUENCE FROM N.A.

MEDLINE=94087159; PubMed=8263493;

Queralt R., de Fabreques-Boixar O., Adroer R., Gene M.,

Gomez-Catalan J., Huguet E., Oliva R.;

Gomez-Catalan J., Huguet E., Oliva R.;

"Direct sequencing of the human protamine Pl gene and application in "Direct sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20123244; PubMed=10659848; Wyckoff G.J., Wang W., Wu C.-I.; Waptoff G.J., Wang W., Wu C.-I.; Rapid evolution of male reproductive genes in the descent of man."; Nature 403:304-309(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                   MEDLINE=91184796; PubMed=2081589;
Domenjoud L., Nussbaum G., Adham I.M., Greeske G., Engel W.;
"Genomic sequences of human protamines whose genes, PRM1 and PRM2,
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=90129065; PubMed=2613245; Krawetz S.A., Herfort M.H., Hamerton J.L., Pon R.T., Dixon G.H.; "Chromosomal localization and structure of the human Pl protamine
                                                                                                                                 MEDINE=85280768; PubMed=4027356;
McKay D.J., Renaux B.S., Dixon G.H.;
"The amino acid sequence of human sperm protamine Pl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "wne nucleotide sequence of a human protamine 1 cDNA.";
Nucleic Acids Res. 15:7639-7639(1987).
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MEDLINE-95074145; PubMed=7983046;
MEDLON J.E., Krawetz S.A.;
"Characterization of a human locus in transition.";
J. Biol. Chem. 269:31067-31073(1994).
        13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Sperm protamine P1 (Cysteine-rich protamine).
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. DubMed=3658707;
SEQUELINE=88015622; PubMed=3658707;
Lee C.-H., Hoyer-Fender S., Engel W.;
The nucleotide sequence of a human pr
                                                                                                                                                                                                      MEDLINE=86296190; PubMed=3527226;
                                                                                                                                                                      5:383-391 (1985)
                                                                                                                                                                                                                                                                                                                        are clustered.";
Genomics 8:127-133(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics 5:639-645(1989).
                                                                 Homo sapiens (Human)
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TISSUE=Testis;
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MEDLINE=2012344; PubMed=10659848;
Wyckoff G.J., Wang W., Wu C.-I.;
"Rapid evolution of male reproductive genes in the descent of man.";
Nature 403:304-309(2000).
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Pfam; PF00266; protamine_Pl; 1.
PROSTIE; PS00048; PROTAMINE_Pl; 1.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.
INIT_MET

DISULFID

S INTERCHAIN (BY SIMILARITY).
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
NCBI_TaxID=9600,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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INTERCHAIN (WITH C-38) (BY
BY SIMILARITY.
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SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: TESTIS.
SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.
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MEDLINE=94141943; PubMed=8308910;
Retief J.D., Winkfein R.J., Dixon G.H., Adroer R.,
Ballabriga J., Oliva R.;
"Evolution of protemine PI genes in primates.";
J. Mol. Evol. 37:426-434(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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EMBL; M60331; AAA63249.1; --
EMBL; M29706; AAA60191.1; --
EMBL; Y00443; CAA66499.1; --
EMBL; U15422; AAC50486.1; --
EMBL; AF215707; AAB29321.2; --
EMBL; AF215707; AAB234620.1; --
EMBL; EC003673; AAH03673.1; --
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RESULT 12
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Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwin Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B. Smith H.O., Venter J.C.;
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INIT MET
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                         or send an email to license@isb-sib.ch)
                                                       modified
                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                   STRAIN-ATCC
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
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NCBI_TaxID=139;
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                                                                                                                                           Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001
                                                                                                                                                                      "Genomic sequence of a Lyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATCENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX. SUBUNIT: CROSS-LINKED BY INTERCHAIN DISULFIDE BONDS AROUND THE DNA-HELIX (BY SIMILARITY).
                                                                                European Bioinformatics Institute.
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PPO0260; protamine P1; 1.

TE; PS00048; PROTAMINE P1; 1.

tosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; nosomal protein; Nucleosome protein.

SY SIMILARITY.

BY SIMILARITY.

CRC64;
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Best Local
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P50594;
01-OCT-1996
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010325;
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SEQUENCE 51 AA; 6444 MW; ACEC7E55B5A8EODA CRC64;
                                                              Eukaryota; Metazoa;
                                                                                              Mago nashi protein
                                                                                                        01-OCT-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                        Hypothetical SEQUENCE 5
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                                                                                                                                                                                                                                                                                                                                                                                                                    polyhedrosis virus genome.";
Virology 229:381-399(1997).
-!- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997
SEQUENCE FROM N.A. TISSUE=Heart;
                                          Gallus.
                                                    Archosauria; Aves;
                                                                         Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                            EMBL; U75930; AAC59074.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ahrens C.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=97271300;
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NCBI_TaxID=164623;
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                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rohrmann G.F.;
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(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
6.3 kDa protein (ORF75).
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                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                       6250 MW;
                                                   Neognathae;
                                                                                              homolog
                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
Veognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                        41.4%;
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44.48;
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annotation
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Pred. No.
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Pred. No. 2.4e+02;
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STRAIDELESSS / Pringsheim;
STRAIDELESSS / Pringsheim;
Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella M.,
Farley J.Y., Schluchter W.M., Chung S., Newmann-Spallart C.,
Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;
"The complete sequence of the cyanelle genome of Cyanophora paradoxa:
the genetic complexity of a primitive plastid.";
(In) Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E.,
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"Nucleotide sequence of the cyanelle DNA from Cyanophora paradoxa.";
Plant Mol. Biol. Rep. 13:327-332(1995).
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STRAIN=LB555 / Pringsheim;
Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg
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NCBL_TaxID=2762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.7%; Score 23; DB 1; Length 26; 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0; Indels
Shi W., Antin P., Flink I.L., Morkin E.;
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nuclear (By simlarity).
-!- SIMILARITY: BELONGS TO THE MAGO NASHI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nuclear protein. — 26 26 26 SEQUENCE 26 As; 3062 MW; AF82470DE9E29230 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Photosystem I reaction centre subunit XII (PSI-M).
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InterPro; IPR004023; Mago nashī.
Pfam; PF02792; Mago nashi; 1.
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Best Local Similarity 100."
Matches 4; Conservative
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7 LRYY 10
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                                                                 2; Indels
31 AA; 3332 MW; D92CA0CE635804D9 CRC64;
                                Score 23; DB 1; I Pred. No. 2.1e+02;
                                                               2; Mismatches
                              Query Match
Best Local Similarity 50.0%;
Matches 4; Conservative
SEQUENCE
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Gaps

1 RIALRYYR 8

23 RLALELYK 30

Search completed: December 19, 2002, 16:19:45 Job time : 6.47059 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

December 19, 2002, 16:16:02; Search time 10.4118 Seconds (without alignments) 110.799 Million cell updates/sec Run on:

US-08-653-294C-40 58 Title: Perfect score:

1 RIALRYYRLAIR 12 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

15911 Total number of hits satisfying chosen parameters:

283224 segs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 60

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical immun		ρ	hypothetical prote	_		nase	1	hypothetical prote					ு	hypothetical prote		Ψ	adenylate isopente	O	g heavy	chain	- uisc	myosin - pig (frag	ivigion	hetical p	ဋ	Iq heavy chain DJ	defensin NP-4 - ra	trypsin (EC 3.4.21
SUMMARIES	ID		AF0546	A69538	H97793	B34224	F97702	G69590	PQ0487	G82620	JS0244	152725	D64786	D71343	866678	D84640	A95335	S78728	PA0057	PH1360	PH1303	PH1335	I61695	I46596	PN0479	B70255	I38222	PH1338	A61014	A61143
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defensin NP-1 - ra defensin R-5 - rat	hypothetical prote hypothetical prote hypothetical prote		O	hypothetical prote cryptogene protein transcription regu	hypothetical prote hypothetical prote
D61014 E61014	S73127 A82598 C85649	B95215 G90716 G64801	D82687 F82409 HSHUP1	B70141 S51909 A84082	T31016 S01179
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30 31	3 8 8 4 8 8	35 36 37	8 6 0 6	4 4 4 4 3 2 1	4 4 5 4

## ALIGNMENTS

	RESULT 1
	IMBP8
	hypothetical immunity region protein 8 - Bacillus phage phi-105
_	C;Species: Bacillus phage phi-105
	A;Note: host Bacillus subtilis
_	C;Date: 20-Aug-1999 #sequence revision 20-Aug-1999 #text change 20-Aug-1999
_	C;Accession: G24521
	R;Cully, D.F.; Garro, A.J.
	Gene 38, 153-164, 1985
	A, Title: Nucleotide sequence of the immunity region of Bacillus subtilis bacteriophage
_	A; Reference number: A91535; MUID: 86056972; PMID: 3934047
-	A; Accession: G24521
	A; Molecule type: DNA
	A;Residues: 1-44 <cul></cul>
	A; Cross-references: GB:M11920; NID:q215477
	C; Comment: This is the hypothetical translation of a sequence that was not reported as
	Query Match 63.8%; Score 37; DB 4; Length 44;
	Beet Local Similarity 54.5%; Pred. No. 3.1; Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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2 IALRYYRLAIR 12 ଚ

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Ay Note: this species almonella enterica subsp. enterica subsp. enterica serovar Typhi
A, Note: this species has also been called Salmonella typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A, Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001
C;Accession: AF0546
R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher th, T.; Connenton, P.; Cronin, A.; Davies, R.M.; Powd, L.; White, N.; Farrar , S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A, Atuchors: Park, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K. A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero A;Reference number: AB0502; PMID:11677608
A;Reference number: AB0502; PMID:11677608
A;Retaus: preliminary
A;Molecule type: DNA
A;Residues: 1.33 < PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08814.1; PID:g16501628; GSPDB:GN00176
C;Genetics:
A;Gene: STY0391 AF0546

Gaps ö Query Match 53.4%; Score 31; DB 2; Length 33; Best Local Similarity 71.4%; Pred. No. 32; Matches 5; Conservative 1; Mismatches 1; Indels 1; Indels

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C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C;Accession: H97793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
Science 293, 2093-2098, 2001
A;Tille: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
                                                                R; Kirsh, A.L.; Groudine,
Genes Dev. 3, 2172-2179,
                                                                                                                                    N;Alternate names: histone H1.10 [misidentification]
C;Species: Gallus gallus (chicken)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #
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A; Residues: 1-52 < KUR>
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A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon, Reference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein AF2305 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
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                                             A; Title: Polyadenylation
                                                                                                              :Accession: B34224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references:
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                        lyadenylation and U7 snRNP-mediated cleavage: number: A91623; MUID:90185195; PMID:2576416
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                                                                                           Groudine, M.; Challoner, P.B
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                 #sequence_revision 07-Jun-1990 #text_change 04-Mar-2000
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70.0%;
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Pred. No.
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Pred. No.
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Query Match
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A;Cross-references: GB:Z99118; GB:AL009126; NID:g2635200; PIDN:CAB14808.1; PID:e1184097; A;Experimental source: strain 168 C;Genetics: A;Gene: ask
                                                                                                                                                                                                    Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Hosono, S.; Hullo, M.F. iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogiwara, A.; Oddega, B.; Park, S. H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanamaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
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A; Residues: 1-27 <KI2>
C; Comment: This sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aspartokinase II attenuator ask - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
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Science 293, 2093-2098,
                                                                                                                                                                            A;Status: preliminary; nucleic acid
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A;Residues: 1-60
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nes 5; Conserv
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Pred. No.
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Pred. No. 1.4e+02;
5; Mismatches 1
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46.6%;
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A;Residues: 1-23 <FUK>
A;Cross-references: GB:X04465
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A,Map position: 18q21.33
C,Keywords: fusion protein
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Matches 5; Conserv
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C;Keywords: chloroplast
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1 MAIRLYRL 8
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Best Local S
Matches 7
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A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Recession: G82620

A;Status: preliminary

A;Mocession: G82620

A;Status: preliminary

A;Residues: 1-40 < SIM>
A;Residues: 1-40 < SIM>
A;Residues: 1-40 < SIM>
A;Residues: 1-60 < SIM>
A;Cross-references: GB:AE004012; GB:AE003849; NID:g9107020; PIDN:AAP84728.1; GSPDB:GN001

A;Residues: 1-70 < SIM>
A;Cross-references: GB:AE004012; GB:AE003849; NID:g9107020; PIDN:AAP84728.1; GSPDB:GN001

A;Residues: M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Salones, M.R.S.; Bueno, M.R.P.; Ferrora, A.J.S.

Briones, M.R.S.; Bueno, M.R.P.; Ferrora, J.A.; Franca, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Undqueira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, B.E.; Laiguchado, M.A.; Maddira, A.M.B.N.; Madeira, M.R.; Marino, C.L.; Marques, M.V.; Martins, E.M.F.; Matukhors: Martins, E.M.F.; Matukhuma, A.Y.; Marxino, C.L.; Mayaki, C.Y.; Fod; Numes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.R. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.S.; de Sa, R.C.; Santelli, R.V.; Sawasak A; Reference number: A59328

A; Contents: annotation

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                                                                                                                                                                                                                                                                                                                                                                                                                           ### Species: Colocasia esculenta (taro)
C;Species: Colocasia esculenta (taro)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-2000
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-2000
C;Accession: PQ048
C;Accession: PQ048
A;Title: Spatial and temporal gene expression patterns occur during Corm development. A;Reference number: PQ0482; MUD:93104679; PMID:1467653
A;Accession: PQ0487
A;Molecule type: protein
A;Residues: 1-25 cCAS
C;Superfamily: plant Kunitz-type proteinase inhibitor
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Pred. No. 1.4e+02;
0; Mismatches 2; Indels
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50.0%; Pred. No. 89;
iive 3; Mismatches
ilarity 71.4%; Pred. No. 86;
Conservative 1; Mismatches
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Best Local Similarity 50.۰۰
نمر 4; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Logal Similarity
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17 RYYAISLR 24
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                                                                                                              RYYRLAI 11
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C;Accession: JS0244
R;Fukuzawa, H.; Uchida, Y.; Yamano, Y.; Ohyama, K.; Komano, T.
Agric. Biol. Chem. 49, 2725-2731, 1985
A;Title: Molecular cloning of promoters functional in Escherichia coli from chloroplast A;Reference number: A90020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Accession: 152725
R;Ji, W.; Qu, G.Z.; Ye, P.; Zhang, X.Y.; Halabi, S.; Ehrlich, M.
R;Ji, W.; Qu, G.Z.; Ye, P.; Zhang, X.Y.; Halabi, S.; Ehrlich, M.
A;Title: Frequent detection of bcl-2/JH translocations in human blood and organ samples
A;Reference number: 152725; MUID:95316863; PMID:7796416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phage lambda ren protein homolog b0542 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: D5479197 #sequence revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: D64786; JN0330; S36858
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.A.; Rose, D.J.; Mau, B.; Shao, Y.
A;Rose, D.J.; Mau, B.; Shao, Y.
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: D64786
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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C;Comment: This sequence is the chimeric product of a translocation mutation.
                 hypothetical BCL2/IGHV mutant fusion protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Feb-1997
(Marchantia polymorpha) chloroplast
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63.6%; Pred. No. 1.5e+02;
iive 0; Mismatches 4;
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A,Molecule type: DNA
A,Residues: 1-27 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27; DB 2;
Pred. No. 1.3e+02
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A;Cross-references: GB:AB000160; GB:U00096; NID:g1786751; PIDN:AAC73643.1; PID:g1786754
A;Experimental source: strain K-12, substrain MG1655
R;Morimyo, M.; Hongo, B.; Hama-Inaba, H.; Machida, I.
Nucleic Acids Res. 20, 3159-3165, 1992
A;Title: Cloning and characterization of the mvrC gene of Escherichia coli K-12 which coli, Reference number: JN0329; MUID:92319648; PMID:1320256
A;Accession: JN0330
                                                                                                                                                                                                                                                                                                                                                    RESULT 14
S66678
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Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochet.
                                                                                                                                             R;Rosenkrands, I.; Hejgaard, J.; Rasmussen, S.K.; Bjorn, S.E. FEBS Lett. 343, 75-80, 1994
A;Title: Serpins from wheat grain
A;Reference number: S43652; MUID:94215711; PMID:8163022
A;Recession: S66678
                                                                                                                                                                                                                                                             serpin - wheat (fragment)
(;Species: Triticum aestivum (common wheat)
(;Decies: Dec-1998 #sequence_revision 05-Dec-1998 #text_change
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change
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C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C;Accession: D71343
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A;Residues: 'MARAGILVVDGKVWRTV',2-45 <MOR>
A;Cross-references: GB:M62732
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                                                                                    A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-43 <ROS>
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A;Experimental source:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Map position: 12.3 min;Superfamily: phage lambda ren protein
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Best Local
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Query Match
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:e: strain Nichols
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71.4%;
44.8%;
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Pred. No. 2.4e+02
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Score 26;
Pred. No.
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3.5e+02;
                      DB 2;
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                         Length 43;
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                                                                                                                                                     C;Genetics.
A;Gene: At2g24780
                                                                                                                                                                                                                                                                                                                                                                R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; I
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-52 <STO>
                                                                                                                                                                                                                                                                                        A; Accession: D84640
                                                                                                                                                                                                                                                                                                        A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                    Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein At2g24780 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Sate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
                                                                                                                                                                                                                                                                      Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                               ;Accession:
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                                                                        Local Similarity 50.
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12 ŘÍRMŘILKLHÍŘ 23
                                    1 RIALRYYRLAIR 12
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                                                                                            44.8%;
                                                                          Score 26; DB
Pred. No. 4.3e
2; Mismatches
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Search completed: December 19, 2002, 16:22:58
Job time : 10.4118 secs

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December 19, 2002, 16:02:26 ; Search time 23.8215 Seconds (without alignments) 55.932 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                            OM protein - protein search, using sw model
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Total number of hits satisfying chosen parameters: 908470 seqs, 133250620 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 US-08-653-294C-39 1 YXXXXRLXER 10 Minimum DB seq length: 0 Maximum DB seq length: 60 Perfect score: Scoring table: Sequence: Searched:

473727

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

A CHIDS2/gcgdata/geneseq\_cembl/AA1980\_DAT:\*

SIDS2/gcgdata/geneseq\_cembl/AA1981\_DAT:\*

SIDS2/gcgdata/geneseq\_geneseqp\_embl/AA1981\_DAT:\*

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SIDS2/gcgdata/geneseq\_geneseqp\_embl/AA1980\_DAT:\*

SIDS2/gcgdata/geneseq\_geneseqp\_embl/AA1991\_DAT:\*

SIDS2/gcgdata/geneseq\_geneseqp\_embl/AA1991\_DAT:\* A\_Geneseq\_101002:\* •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	HLA-B2702 CTL modu	HLA-B2702 CTL modu	Peptide B2702.84-7	Peptide B2702.84-7	Immunomodulatory p	Immunomodulatory p	Immunosuppressive	HLA-B2702 84-75-84	HLA-B7.84-75-84 Pa	HLA-B2702 CTL modu
		QI.	AAR92910	AAR92908	AAW33791	AAW33793	AAW47266	AAW47270	AAY72478	AAR95428	AAR95415	AAR92909
		DB	16	16	13	19	19	13	22	16	16	16
		Match Length DB	20	20	20	20	10	10	10	20	20	20
d	Query	Match	74.2	74.2	74.2	74.2	71.0	71.0	71.0	71.0	71.0	71.0
		Score	23	23	23	23	22	22	22	22	22	22
	Result	No.	-	N	e	4	ഹ	9	7	œ	6	10

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1 May 1 May

Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient host

Clayberger C, Krensky AM, Parham P;

WPI; 1995-358582/46.

HLA-B2702 CTL modu	HLA-B7 CTL modulat	HLA-B2702 CTL modu	Immunomodulating d	Immunomodulating d	Peptide B7.84-75/7	B2702	Peptide B7.84-75/7	Immunomodulatory p		CD4-variant genera	CD4-variant 3. Ho	Domain 1 from inte	Chimaeric peptide	Domain 1 sequence	Human hKv1-4 N-ter	Novel human diagno	Novel human diagno	Cell population st	Peptide #8298 enco		Human brain expres	Human bone marrow	Peptide #8595 enco	Human peptide enco	Helix-loop-helix m	Helix-loop-helix m	Human secreted pro	Human immune/haema	Human secreted pro	Human secreted pro		Drosophila melanog		Peptide #1539 enco
L6 AAR92911		16 AAR92907	19 AAW33778	19 AAW33779	.9 AAW33790	.9 AAW33792		.9 AAW47268	.9 AAW47272	19 AAW85996	19 AAW85959	14 AAR34561	17 AAR97473		21 AAB36239			2 AAB74582		22 ABB24987	2 AAM61652	2 AAM74444		3 ABG44333			3 ABB94081		0 AAY13207			ABB6697	ABB28	2 ABB34033
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11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702. HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)). (STRD ) UNIV LELAND STANFORD JUNIOR. AAR92910 standard; peptide; 20 AA. 95WO-US04349 94US-0222851 16-MAY-1996 (first entry) W09526979-A1. 05-APR-1995; 05-APR-1994; 12-0CT-1995. Synthetic. AAR92910; RESULT 1 AAR92910 

AAR83061-R83085,

AAR83090-R83096 and AAR92907-R92913 represent fra histocompatibility complex (MHC) antigens. This

fragments

Example 15; Page 36; 80pp; English

of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)

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            AAR83061-R83085, AAR83090-R83096 and AAR92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
administration for current modulate (or inhibit) the a of the patient.
                                                                                                                                                                                     Example 15; Page
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                                                                                                                                                                                                                                                                                WPI; 1995-358582/46
                                                                                                                                                                                                                                                                                                             Clayberger C,
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                                                                                                                                                                                                                                     hosts
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                                                                                                                                                                                                                                   acceptance period of transplants from MHC unmatched - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modulating peptide (B2702.84-75(T)/75-84).
                                                                                                                                                                                                                                                                                                              Krensky
                                                                                                                                                                                                                                                                                                                                                                           94US-0222851
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                                                                                                                                                                                     36; 80pp; English.
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Query Match Best Local Similarity

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                                                  CC immunomodulating activity. A peptide-type compound or variant is claimed CC which has immunomodulating activity, including the N-terminal acylated CC and/or C-terminal amidated or esterified forms of up to 60 amino acids, CC where the peptide-type compound comprises the formula; A-B, where A, B = CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = CC D, S or N; aa79 = R or G; aa80 = I or N; aa81 = a bydrophobic or Small amino acid; aa82 = R or L; aa83 = G or R; and a represents amino acid. The sequence in the brackets may optionally be absent or truncated CC amino acid sequences related to a Class I HLA-B alphal domain (positions CC 19-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from CC used in combination with antigenic apptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection CC fransplants or for treating autoimmune diseases, e.g. diabetes, CC used for detection and diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptides AAW33784-98 and AAW33778-9 were assayed for their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New immunomodulating dimer peptide(s) - based alpha-1 domain, used for preventing rejection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunomodulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YXXXXRLXER 10
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Pred. No. 9;
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Novel immunomodulatory peptide-type compound - useful for inhibiting
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                                                                                                                                                                                                                                                                                                                                                                                                   1..10
/note= "at least one of the amino acids is the
                                                                                                                                                                                                                                                   Immunomodulator; Class I HLA-B alpha-1 domain; inhibition; transplant rejection; treatment; autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                  AAW47266 standard; peptide; 10 AA.
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                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                            Immunomodulatory peptide.
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Misc-difference 1
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                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                            AAW47266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           impunomodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-771) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa92 = R or G; aa80 = 1 or N; aa81, aa84 = a hydrophobic or acid. The sequence in the brackets may optionally be absent or truncated acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise an ino acid sequences related to a Class I HLB alphal domain (positions 79-84). They can be used to inhibit cytocoxic T-lymphocytes (CTL) from undeasirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatcoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
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                                                                                                                                                                                                                                                                                                                                        Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
rejection.
                                                                                                                                                                                                                                                                                                          Peptide B2702.84-75T/75-84T tested for immunomodulating activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 23; DB 19; Length 20;
Pred. No. 9;
0; Mismatches 5; Indels
  5; Indels
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beulow R, Clayberger C, Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                    AAW33793 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 19; 41pp; English.
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50.0%;
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Best Local Similarity 50.0
Matches 5; Conservative
Conservative
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                                         1 YXXXXRLXER 10
                                                                              1 YRLATRINER 10
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                                                                                                                                                                                                                                                                     19-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9744351-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAY-1997;
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5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                           AAW33793;
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1 YRLATRINER 10

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               15-MAY-2000; 2000WO-EP04338
                                        28-DEC-2000
                                                                 WO200079263-A2
                                                                                          Unidentified
                                                                                                               Immunosuppressive; allograft rejection; topological parameter; physico-chemical parameter; in silico screening; pharmaceutical; cosmetic; agrochemical; biomaterial; veterinary application.
                                                                                                                                                                                             24-APR-2001
                                                                                                                                                                                                                                            AAY72478 standard; peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptides using the D-form amino acids are more effective immunomodulators than their diastereomers or enantiomers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               the treatment of autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transplant rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel immunomodulatory peptide-type compound - useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-018220/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clayberger C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transplant rejection; treatment; autoimmune disease.
                                                                                                                                                                    Immunosuppressive peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                              10 AA;
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Krensky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0651650
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                                                                                                                                                                                                                                                                                                                                                                        71.0%;
50.0%;
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                                                                                                                                                                    2702.84-75, to prevent allograft rejection
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of function, and selecting the second subset from physico-chemical parameters, determining their value parameters based on the values of function, such that each second subset is more closely associated with the activity than the first subset. The selected physico-chemical parameters are useful for developing criteria for screening candidate molecules and are suitable for use in silico screening of compounds. The compounds may be used in pharmaceuticals, cosmetics, agrochemicals, biomaterials and in veterinary applications. It is also useful as an antibiotic or antifungal agent. The present sequence is an immunosuppressive peptide, 2702.475 (also referred as D2702.75-84), identified by in silico screening. The immunosuppressive activity of the peptide that prevents allograft rejection is tested in a heterotopic allograft model of mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; AI B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
WPI; 1995-194027/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytolysis; antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLA-B2702 84-75-84 palindrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a method for identifying physico-chemical and/or topological parameters associated activity. The method involves selecting the first subset i predetermined set of physico-chemical parameters, determin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying active candidate molecules on the basis of selected physico-chemical parameters, for in silico screening of compounds useful in pharmaceuticals, cosmetics, veterinary applications and
                                                        Clayberger C,
                                                                                                                                                                                                                                                                                            18-MAY-1995.
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                                                                                                                                                                         10-NOV-1993;
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                                                                                                                (STRD ) UNIV
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
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                                                                                                                LELAND STANFORD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                        Krensky AM
                                                                                                                                                                         93US-0150493
                                                                                                                                                                                                                                    94WO-US12985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                presenting cell.
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Pred. No. 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hsc70; APC;
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HLA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; rcell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell. Mismatches (STRD ) UNIV LELAND STANFORD JUNIOR. AAR95415 standard; peptide; 20 AA Example; Page 12; 29pp; English . 0 71.0%; 93US-0150493 HLA-B7.84-75-84 Palindrome. 12-NOV-1996 (first entry) Krensky AM; 5; Conservative WPI; 1995-194027/25. Query Match Best Local Similarity 1 YXXXXRLXER 10 1 YRLAIRLNER 10 20 AA; Clayberger C, WO9513288-A1 10-NOV-1994; 10-NOV-1993; 18-MAY-1995. Synthetic. Sequence Matches ઠ 셤 

AAR95413, and AAR95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence can be used to isolate the protein p74 from a T-cell lysate. P74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Haso70. P74 is found in a limited number of cell types, but is particularly expressed on B and T cells. P74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-44 (see AAR95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and chermining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular containing T-cells and antigen presenting cells (APCS), by adding the mix the actracell so the part of the compound and containing T-cells and antigen presenting cells. adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand Score 22; DB 16; Length 20; Pred. No. 18; 0; Mismatches 5; Indels 71.0%; Best Local Similarity 50.0 Matches 5; Conservative 1 YXXXXRLXER 10 1 YGRLNRLSER 10 20 AA; Sequence Query Match RESULT 10 AAR92909 ð 용 ö AAR95413, and AAR95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the Hah-B2702 84-75-84 palindrome. These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein associated with T-cell lactivation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable coll with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see AAR95416), induces calcium influx, and inhibits of particular of the protein the compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCs), by Gaps Compsns. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS. adding to the mix the extracellular portion of 974, in an amount sufficient to compete with p74 for the binding of the p74 ligand ö Score 22; DB 16; Length 20; Pred. No. 18; 5; Indels

Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702. HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)). AAR92909 standard; peptide; 20 AA. 16-MAY-1996 (first entry) WO9526979-A1. Synthetic.

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Gaps

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Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient Clayberger C, Krensky AM, Parham P; (STRD ) UNIV LELAND STANFORD JUNIOR. Example 15; Page 36; 80pp; English. 95WO-US04349, 94US-0222851 WPI; 1995-358582/46. 05-APR-1995; 05-APR-1994; 12-OCT-1995. 

AAR83061-R83085, AAR83090-R83096 and AAR92907-R92913 represent fragments of class I major histocompatibility complex (WHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the

Compsns. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.

Example; Page 18; 29pp; English.

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Matches 5; Conserv
                                                                                                                                               AAR83061-R83085, AAR83090-R83096 and AAR92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                            Example 15; Page 36; 80pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clayberger C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLA-B2702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR92911 standard; peptide; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                               patient.
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Similarity 5; Conserv
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                                                                                      20
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                acceptance period of transplants from MHC unmatched - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                      ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modulating peptide (B2702.84-75/84-75).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Krensky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94US-0222851.
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50.0%;
                  71.0%;
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Score 22; DB
Pred. No. 18;
0; Mismatches
  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 22; DB Pred. No. 18; 0; Mismatches
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18;
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                                        Length 20;
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    Indels
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RESULT 13
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                                                                                                                                                                                         Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                              AAR83061-R83085, AAR83090-R83096 and AAR92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B7. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B7.
                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                  of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                       16-MAY-1996
                                                                         AAR92907
                                                                                                                                                                                                                                                                                                                                                                                                                        Example 15; Page 36; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clayberger C,
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                                                                                                                                                                                       Similarity
5; Conserv
                                                                         standard;
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                                                                                                                                                                                          Conservative
                      (first entry)
                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Krensky AM,
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                                                                                                                                         10
                                                                       peptide;
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                                                                                                                                                                                         0
                                                                                                                                                                                                     Score 22;
Pred. No.
                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                     18;
                                                                                                                                                                                                                 16;
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                                                                                                                                                                                         Indels
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HLA-B2702 CTL modulating peptide (B2702.84-75/75-84)

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treating autoimmune diseases
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                                                       Clayberger C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                   WPI; 1998-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YXXXXRLXER 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 AA;
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                                                       Beulow R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW33779;
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                                                                                                                                                                                                                                                                                                                                                                                AAR83061-R83085, AAR83090-R83096 and AAR92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapettic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLS)
          Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                 Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.0%; Score 22; 50.0%; Pred. No.
                                                                                                                                                                                                           (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                        Example 15; Page 36; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW33778 standard; peptide; 20 AA.
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                                                                                                                                                       95WO-US04349
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                                                                                                                                                                                                                                          Krensky AM,
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                                                                                                                                                                                                                                                                     WPI; 1995-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YXXXXRLXER 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the patient
                                                                                                                                                                                                                                         Clayberger C,
                                                                                                                                                    05-APR-1995;
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                                                                                               W09526979-A1
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                                                                                                                           12-OCT-1995
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                                                                  Synthetic.
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This sequence represents a specifically claimed immunomodulating dimer peptide of the invention. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = B or V; aa37 = L). S or N; aa79 = B or G; aa80 = I or N; aa81, aa84 = B or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = B or V; aa87 = D, S or N; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cyctoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in virtor They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proteins of interest to activate CTLs. They can also inhibit the proteins of for preventing rejection of transplants or for treating autoimmune and the process of the preventing autoimmune and the process or the process of the preventing rejection of transplants or for treating autoimmune and the process or the process of the preventing rejection of transplants or for treating autoimmune and the process or proces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                               New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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(STRD ) UNIV LELAND STANFORD JUNIOR.
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Search completed: December 19, 2002, 16:19:06 Job time : 24.8235 secs
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                                                                                                                                                                                                                                                 This sequence represents a specifically claimed immunomodulating cdimer peptide of the invention. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal cc acjuated and/or C-terminal amidated or esterified forms of up to 60 cc amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or C; v; aa77 = D; S or N; aa79 = R or G; aa80 = I or N; aa81 = aa84 = a cc hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be cabsent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B calphal domain (positions 79-84). They can be used to inhibit cytotoxic CT -lymphocytes (CTL) from undesirably attacking cells in a host or in CC proteins of interest to activate CTLs. They can also inhibit the products or preventing rejection of transplants or for treating autoimmune classes, e.g. diabetes, rheumatoid arthritis and lupus erythematosis.
                                                                                                                                                              Query Match 71.0
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases
                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 16; Page 35; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-086530/08
                                                                                                                        1 YXXXXRLXER 10
                                                                                YRLAIRLNER 10
                                                                                                                                                                                                                                                 20 AA;
                                                                                                                                                                                   71.0%;
                                                                                                                                                                ; Score 22; DB;
; Pred. No. 18;
0; Mismatches
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                                                                                                                                                                   5
                                                                                                                                                                                                         Length 20;
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geospiza sc
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rhizobium m
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Q8wm91 cactospiza
Q8wm90 certhidea o
Q8wm89 platyspiza
Q8wm88 melanospiza
                    96617 echinococcu
Q982h9 rhizobium l
                                                 Q36270 zea mays (m
Q36278 zea mays (m
Q9hr17 halobacteri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-S. aureus (strain Mus0), and S. aureus (strain N315);
MEDLINE-21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehiga M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315).
Bacteria, Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.2%; Score 23; DB 16; Length 56; 50.0%; Pred. No. 43; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Complete proteome.
SEQUENCE 56 AA; 6474 MW; FADB3071F92F683D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUNAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein SAV1287.
SAV1287 OR SAI129.1 OR SAS037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
Q86528
Q96617
Q96219
Q36270
Q913228
Q91328
Q913328
Q313328
Q31332
Q81332
Q81332
Q85055
Q85055
Q85067
Q91873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lancet 357:1225-1240(2001).
EMBL; AP003361; BAB57449.1; -.
EMBL; AP003133; BAB42382.1; -.
                                                                                                                                                     Staphylococcus.
NCBI_TaxID=158878, 158879;
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nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
 1 YXXXXRLXER 10
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 Query Match
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 910660
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Q94374 caenorhabdi
Q63988 rattus norv
Q59ky0 aurelia aur
Q9vez8 drosophila
Q9uh70 agrobacteri
Q27979 archaeoglob
Q9y188 priapulus c
Q95m32 rhizobium l
Q92528 listeria in
Q92528 listeria in
Q95m19 lissomyema
Q9bm15 spongilla l
Q9bm76 glardia lam
Q9bm76 glardia lam
Q9bm76 glardia lam
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                                                                                                                December 19, 2002, 16:14:32; Search time 17.6471 Seconds (without alignments) 116.760 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                5.1.3
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                              671580 seqs, 206047115 residues
              GenCore version
Copyright (c) 1993 - 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                 OM protein - protein search, using sw model
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Q99UBN9
Q639BN
Q639B
Q9NKY0
Q9VEZB
Q9VI8B
Q98M32
Q92SZB
Q98M19
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Q9BM75
Q9BM74
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
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sp_organelle:*
sp_phage:*
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sp_bacteriap:*
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Match Length
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Maximum DB seq length: 60
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110...
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Best Local
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Q94374;
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Zeke T., Gergely P., Dombradi V.;

"The catalytic subunits of Ser/Thr protein phosphatases from Caenorhabditis elegans: A biochemical and molecular biologics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                   EMBL; Z77735; CAB01294.1; HSSP; P08129; 1FJM.
                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                            survey.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PP1-like Ser/Thr protein phosphatase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000569; HECT_domain.
Pfam; PF00632; HECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF009341; AAC39580.1; EMBL; AJ001113; CAA04540.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hennies H.C., Buer "Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98126441; PubMed=9465301; Kishino T., Wagstaff J.; "Genomic organization of the UBE3A/E6-AP gene and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01.MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
E6_AP ubiquitin-protein ligase (Fragment).
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                                                                                                      SIMILARITY: BELONGS TO
                                                                                                                                                                         nitted (JUL-1996) to CATALYTIC ACTIVITY:
                                                                                                                                         PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                              _TaxID=6239;
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IPR004844; S/T_phosphtse
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ДД;
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the E6-AP gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25
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40.0%;
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                                                                                                                                                                         A PHOSPHOPROTEIN
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                                                                                                      THE
                                                                                                                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20; DB pred. No. 2.1e
1; Mismatches
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                                                                                                      FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Fragment).
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n patients with Angelman
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                                                                                                         PHOSPHATASES
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RESULT 5
Q9NKY0
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Best Local
                                                                                                                                               01-OCT-2000
01-OCT-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q63988;
Q63988;
01-NOV-1996
SEQUENCE FROM N.A.
Sakaguchi M., Takahashi Y.,
"Aurelia aurita neoScox-1 homeodomain protein,
"Submitted (JAN-2000) to the EMBL/GenBank/DDBJ c
EMBL, AB037147; BAA89786.1; -.
HSSP; P14653; 1B72.
                                                                                                                                                                                   Q9NKY0;
                                                                                                                                                                                                                                                                                                                                                                                                                  Iimura T., Oida S., Takeda K., Maruoka Y., Sasaki S.; "Changes in homeobox-containing gene expression during formation induced by bone morphogenetic protein."; Biochem. Biophys. Res. Commun. 201:980-987(1994). EMBL; S71284; AAB31004.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
                                                                                                      Eukaryota; Metazoa;
                                                                                                                                      NeoScox-1 homeodomain
                                                                                                                                                                                                                                                                                                                                                           DNA-binding; Homeobox; Nuclear NON_TER 1 1 1 NON_TER 25 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Iron; Manganese.
NON_TER 1 1
NON_TER 24 24
SEQUENCE 24 AA; 2787 MW;
                                                                                            Aurelia
                                                                                                                  Aurelia aurita (moon
                                                                                                                              NEOSCOX-1.
                                                                                                                                                                                                                                                                                                                                                SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001356; Homeob
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=BONE MORPHOGENETIC PROTEIN-IMPLANTED MEDLINE=94271262; PubMed=7911662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
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                                                                              NCBI_TaxID=6145;
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                                                                                                                                              ) (TrEMBLrel. 15, 0) (TrEMBLrel. 15, 12) (TrEMBLrel. 20, 12)
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                                                                                                                                                                                                                                                                                                                                               3111 MW;
                                                                                                     Cnidaria; Scyphozoa; Semaeostomeae; Ulmaridae;
                                                                                                                  jelly).
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80.0%;
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Last sequence update)

Last annotation updat

in (Fragment).
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Pred. No. 2.5e
1; Mismatches
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Pred. No. 2.6e+02;
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databases.
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Amanatides P.G., Scherer S.E., Lip P.W., Brahurner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Ragers Y. H.C., Blazel, R.G., Champen M., Pfeiffer B.D.,
Rh Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Rank R.M., Basun A., Baxendale J., Baytaktaroglu L., Beasley B.M.,
Ballew R.M., Basun A., Baxendale J., Baytaktaroglu L., Beasley B.M.,
Rallew R.M., Basun D.A., Butler H., Cadlews P., Entersor P.,
Bartis K.C., Busam D.A., Butler H., Cadlews P., Chandra I.,
Rank Burtis K.C., Busam D.A., Butler H., Cadlews P., Chandra I.,
Rank Burtis K.D., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Rh Burtis K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman W.,
Rh Geblos B., Delcher A., Dong R., Dougher S., Plunkov B.C., Dun P.,
Rh Cong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Houtin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
Alali M., Kalush F. Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Ju X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Murtho G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Wurphy B., Murphy L., Murny D.M., Nelsen D.R.,
Shirekas R., Tector C., Turner R., Venter E., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Williams S.M., Woodag T., Woller E., Wang S., Yao Q.A.,
Williams S.M., Woodag T., Woller E., Wang S., Yao Q., Zhan B., Zhan M., Zhang G., Zhan W., Zhang G., Zhan X., Zhan C., Zhan H., Zhang G., Zhan X., Zhan K., 
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                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                     Score 19; DB 5; Length 38;
Pred. No. 3.8e+02;
0; Mismatches 1; Indels
                                                                           PROSITE; PS50071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
NON_TER 1 1 1 1 SEQUENCE 38 A8, 4994 MW; D78CC1FDCAE08B63 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                        52 AA.
                                                                                                                                                                                                     0; Mismatches
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Intérpro, IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
PRINTS; PR000024; HOMEOBOX.
Probom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                     61.3%;
80.0%;
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                                                                                                                                                                  Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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MEDLINE=21608551; PubMed=11743194;
MEDLINE=21608551; PubMed=11743194;
MOOING B., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
Science 294:2323-2328(2001).
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"The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=2160850; PubMed=11743193; Monks D.E., Kitajima J.P., Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palnieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein Atu0815.
ATU0815 OR AGR C 1494.
AGROSCHTUM Tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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80.0%; Pred. No. 5.2e+02;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Score 19; DB 5; Length 52;
Pred. No. 5.1e+02;
0; Mismatches 1; Indels
                                                                                                                             FIYBASE, FBGN0001117; pnr.
InterPro; IPR00164; hRIP like.
InterPro; IPR00169; Znf GATA.
PRINTS; PR00619; GATAZNFINGER.
PROSITE; PS00344; GATA_ZN FINGER 1; 2.
PROSITE; PS50114; GATA_ZN FINGER 2; 2.
SEQUENCE 52 AA; 6046 MW; 6E43775E6EEB4346 CRC64;
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Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.; The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 AA.
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SEQUENCE 53 AA; 6196 MW; DFBAE1C75C5
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                                                                                                                                                                                                                                                                                                                                                                                                            61.3%;
80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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RESULT
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Best Local S
Matches 4
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STRAIN=VC-16 / DSM 4304 / ATCC 49558;

Klenk H.-P., Clayton R.J., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Kirkness B.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Kirkness B.F., Dougherty B.A., McKenney K., Adams M.D., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason P.W., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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01-JAN-1998
01-MAR-2002
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027979;
                                                                                                                 "Hox genes in brachiopods and priapulids and Nature 399:772-776(1999).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILAR
  Pfam; PF00046; homeobox; 1
                                                                    EMBL; AF144888; AAD40644.1;
HSSP; P02833; 9ANT.
                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=99318125; PubMed=10391241;
de Rosa R., Grenier J.K., Andreeva
Carroll S.B., Balavoine G.;
                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                     Priapulus caudatus.
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01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9Y188;
01-NOV-1999
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Nature 390:364-370(1997).
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Archaea; Euryarchaeota; Archaeoglobi;
Archaeoglobaceae; Archaeoglobus.
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                    InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH_repre
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Last annotation updat
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Pred. No.
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                                                                                                                                                                    protostome evolution.";
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Best Local S
Matches 4
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                                                                  Q925Z8 PRELIMINARY; PRT; 58 AA.
Q925Z8;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation updat.
Hypothetical protein lin1746.
LIN1746 OR LIN1251.
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01-OCT-2001
01-OCT-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                             Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., N Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing & Mesorhizobium loti.";
                                       Listeria innocua.
Bacteria; Firmicutes; E
Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical MSL0755.
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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PROSITE; PS50071; HOMEOBOX_2; 1.
DNA-binding; Homeobox; Nuclear protein.
NON_TER 1
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SEQUENCE FROM N.A.
STRAIN=CLIP 11262 / SEROVAR 6A;
                                                                                                                                                                                                                                                                                    Hypothetical
SEQUENCE 5
                                                                                                                                                                                                                                                                                                        DNA Res. 7:331-338(2000).
EMBL; AP002995; BAB48281.1;
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MEDLINE=21082930; PubMed=11214968;
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                             NCBI_TaxID=1642;
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                                                                                                                                                                                                                                                                                     58 AA;
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. (TrEMBLrel. 18, La
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C5BEBDC3FF061623 CRC64;
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Pred. No. 5.7e+02;
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M., Matsuno P
Sugimor
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K., Kimura
                                                      Bacillales;
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Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
Haplosclerida; Spongillidae; Spongilla.
NCBL_TaxID=6055;
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EMBL; AY013993; AAGS9967.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arkhipova I., Meselson M.;
"Transposable elements in sexual and ancient asexual taxa.";
Prrorn Natl. Acad. Sci. U.S.A. 97:14477(2000).
EMBL; AY013917; AAG59902.1; -.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11. LINE-like reverse transcriptase (Fragment).
Glardia lamblia (Glardia intestinalis).
Eukaryota, Diplomonadida, Hexamitidae, Giardiinae; Giardia.
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NCBI_TaxID=5741;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
LINE-like reverse transcriptase (Fragment).
Giardia lamblia (Giardia intestinalis).
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Pred. No. 5e+02;
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TRANSPOSON=LRT-L3 RETROTRANSPOSON;
MEDLINE=20570504; PubMed=11121049;
                                                                                                                  TRANSPOSON=GRT-G4 RETROTRANSPOSON;
MEDLINE=20570504; PubMed=11121049;
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80.0%;
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           Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
A Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve B., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
A Gautier L., Gobel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
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Comparative genomics of Listeria species.",
EMBL, ALS96169, CAC96977.1;
REMBL, ALS96169, CAC96482.1; -.
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"Transposable elements in sexual and ancient asexual taxa.";
Proc. Natl. Acad. Sci. U.S.A. 97:14473-14477(2000).
EMBL; AY013983; AAGS9959.1; -. RNA-directed DNA polymerase.
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SEQUENCE 58 AA, 6804 MW; 49412202B2B80E31 CRC64;
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Gypsy-like reverse transcriptase (Fragment).
Spongilla lacustris (Freshwater sponge).
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MEDLINE=20570504; PubMed=11121049;
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Copyright (c) 1993 - 2002 Compugen Ltd.
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December 19, 2002, 16:03:12 ; Search time 4.55882 Seconds (without alignments) 90.980 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-08-653-294C-39 Title: Perfect score:

1 YXXXXRLXER 10 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

5116 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 60

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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34 14 45.2 51 1 AFPI SINAL 35 14 45.2 54 1 SX13_XENIAN 36 14 45.2 55 1 PHNS_DESCH 39 14 45.2 55 1 PHNS_DESCH 39 14 45.2 55 1 VALD_ECOLIN 40 14 45.2 56 1 YGKD_STRDIAN 41 14 45.2 58 1 IHH_DANGE 42 14 45.2 58 1 IHH_DANGE 43 14 45.2 58 1 IHH_DANGE 44 14 45.2 58 1 IHH_DANGE 45 14 45.2 58 1 IHH_DANGE 45 14 45.2 58 1 IHH_DANGE 45 14 45.2 58 1 IHH_DANGE 46 14 45.2 58 1 IHH_DANGE 47 14 45.2 58 1 IHH_DANGE 48 14 45.2 58 1 IHH_DANGE 49 14 45.2 58 1 IHH_DANGE 40 01-JAN-1990 (Rel. 13, Last sequence up 40 01-JAN-1990 (Rel. 13, Last sequence up 41 14 45.2 58 1 IHH_DANGE 45 11 APSQL 46 11 APSQL 46 11 APSQL 47 11 APSQL 48 11 AP	AGRP_LUFCY  AGRP_LUFCY  AC P56569,  DT 15-DEC-1998 (Rel. 37, La  DT 15-DEC-1998 (Rel. 37, La  DT 15-DEC-1998 (Rel. 37, La  DE 6.5 kDa arginine/glutam  OS Luffa cylindrica (Smooth  OC Eukaryota, Viridiplantae  OC Eukaryota, Viridiplantae  OC Eukaryota, Viridiplantae  OC Eukaryota, Viridiplantae  OC NCBI_TaxID=3670;

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P02673; P14464;

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01-NOV-1990 (Rel. 16, 1

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P19294;
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"Primary structure of 6.5k-arginine/glutamate-rich polypeptide for the seeds of sponge gourd (Luffa cylindrica).";
Biosci Biotechnol Biochem. 61:94-988(1997).
-i- FUNCTION: STORAGE PROTEIN WHICH PROVIDES NITROGEN AND CARBON RESERVES DURING GERWINATION AND SEEDLING GROWTH.
-i- MASS SPECTROMETRY: MW=5693.39; METHOD=MALDI.
                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
 Canis
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Hypothetical 6.1 kDa protein.
Thermoproteus tenax virus 1 (strain KRA1) (TTV1)
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P08804;
01-NOV-1988
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          SEQUENCE FROM N.A.

MEDLINE=86259728; PubMed=3014529;

Willey R.W., Rutledge R.A., Dias S., Folks T., Theodore T.,

Willey R.W., Rutledge R.A., Dias S., Folks T., Theodore T.,

Buckler C.E., Martin M.A.,

"Identification of conserved and divergent domains within the

"Identification of conserved and divergent domains within the

envelope gene of the acquired immunodeficiency syndrome retro

proc. Natl. Acad. Sci. U.S.A. 83:5032-5042(1966).
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SEQUENCE
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MOD_RES
CONFLICT
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(ALPHA, BETTA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONE
-!- MISCELLANEOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGERED
THROMBIN, WHICH CLEAVES FIBRINGEPTIDES A AND B FROM ALPHA & BE
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
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"The nature of the peptides released from canine fibrinogen.";
Biochem. Biophys. Res. Commun. 14:555-558(1964).
-i- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                          Viruses; Retroid
NCBI_TaxID=11698;
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Blomback B., Blomback M., Grondahl N.J.;
"Studies on fibrinopeptides from mammals.";
Acta Chem. Scand. 19:1789-1791(1965).
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Birken S., Wilner G.D., Canfield R.E.;
"Studies of the structure of canine fibrinogen.";
Thromb. Res. 7:599-610(1975).
                                                                                                                                                                                                                                        Human immunodeficiency virus type 1 (New York-5 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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PIR; A05296;
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Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vulpes vulpes (Red fox).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-16.
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3; Conserv
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                                                                                                                                                                                                                                                                                                              (Rel. (Rel. (Rel. 3)
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A05296.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                       09, Created)
09, Last sequence 35, Last annotation
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Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7236
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                                                                                                                                                                                                                                                                                                                annotation update) (Fragment).
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FIBRINOPEPTIDE A.
PHOSPHORYLATION (IN SOME
N -> D (IN REF. 2).
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Pred. No.
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                                                syndrome retrovirus.";
THE ENDOPLASMIC
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Canis.
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Pred. No.

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Best Local Similarity 60.0
Matches 3; Conservative
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                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buckler C.E., Marrin M.A.;
"Identification of conserved and divergent domains within the
envelope gene of the acquired immunodeficiency syndrome retrovirus.";
Proc. Natl. Acad. Sci. U.S., 83:5038-5042[1986].
-! FUNCTION: ACTS IN THE DEGRADATION OF CD4 IN THE ENDOPLASMIC
RETICULUM AND IN THE ENHANCEMENT OF VIRION RELEASE PROM THE PLASMA
MEMBRANG OF INFECTED CELLS.
-! SUBCELLULAR LOCATION: Membrane-bound.
RETICULUM AND IN THE ENHANCEMENT OF VIRION RELEASE FROM THE PLASMA
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-86259728; PubMed=3014529;
MILLEY R.W., Rutledge R.A., Dlas S., Folks T., Theodore T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16; DB 1; Length 45;
Pred. No. 3.6e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 45 AA; 5166 MW; 2AA46D116BB624F7 CRC64;
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01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
VPU protein (U ORF protein) (Fragment).
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                        MEMBRANE OF INFECTED CELLS.
-!- SUBCELLULAR LOCATION: Membrane-bound.
                                                                                                                                                                                                                                                                                                         EMBL; K03346; AAB02406.1; -. HSSP; P19554; 1VPU. HIV; K03346; VPUSNYS. InterPro; IPR002094; Vpu. Pfam; PF0558; Vpu; 1. Transmembrane; AIDS.
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HIV; K03347; VPU523.
InterPro; 1PR002094; Vpu.
Pfam; PF00558; Vpu; 1.
Transmembrane; AIDS.
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Matches 3; Conservative
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9 RIRER 13
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P08805;
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VPU_HV1Z3
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIDS Res. Hum. Retroviruses 5:121-129(1989).
-!- FUNCTION: ACTS IN THE DEGRADATION OF CD4 IN THE ENDOPLASMIC RETICULUM AND IN THE ENHANCEMENT OF VIRION RELEASE FROM THE PLASMA MEMBRANE OF INFECTED CELLS.
-!- SUBCELLULAR LOCATION: Membrane-bound.
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Srinivasan A., York D., Butler D. Jr., Jannoun-Nasr R., Getchell J., McCormick J., Ou C.Y., Myers G., Smith T., Chen E.; "Molecular characterization of HIV-1 isolated from a serum collected generation of hybrid HIV-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1 (Zaire HZ321 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2104;
[1]
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NON TER 1 1 SEQUENCE 58 AA; 6789 MW; 40EE98A77BB3DACE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                          01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
VPU protein (U ORF protein) (Fragment).
                                                                                                                                                                                                                                                 58 AA.
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                                      Mismatches
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MEDLINE=89228766; PubMed=2713163;
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HSSP; P19554; 1VPU.
HIV; M15896; VPU$5321.
Interpro; IPR002094; Vpu.
Pfam; PF00558; Vpu.; 1.
Transmembrane; AIDS.
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60.0%;
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Best Local Similarity
                                                                                   6 RLXER 10
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9 RIRER 13
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22 RIRER 26
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P08806;
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DB 1; Length 45;

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Best Local
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                                                                  Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Retchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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                                                                                                                                                                                                                                                                                                                                                 STRAIN=VC-16 / DSM 4304 / ATCC 49558; MEDLINE=98049343; PubMed=9389475;
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
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30-MAY-2000
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EMBL; AE000053; AAG34754.1; -.
InterPro; IPR001911; Ribosomal S21.
PROSITE; PS01181; RIBOSOMAL S21; FALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Nucleic Acids Res. 28:3278-3288(2000)
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Andrade M.A., Doerks T., Sanchez-Pulido
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97105885; PubMed=89
Himmelreich R., Hilbert H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=ATCC 29342 /
reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaeoglobaceae; Archaeoglobus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Re-annotating the Mycoplasma pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yuan Y.P.,
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                      complete genome sequence of the hyperthermophilic, sulphate-
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  archaeon Archaeoglobus fulgidus.";
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(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein AF0569.
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PubMed=8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome. 7515 MW; 30D87DCF4635F003 CRC64;
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Pred. No. 4.8e
1; Mismatches
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(See http://www.isb-sib.ch/announce/
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B., Suyama
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RESULT 11 YF07\_HAEI

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Best Local
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SMART; SM00070; GLUCA; 1.
SMART; SM000260; GLUCAGON; 1
                                                                                                                                                                                                                                                                                                     MEDLINE=90259845; PubMed=2344700,
Gossen D., Buscail L., Cauvin A., Gourlet P., Gossen D., Vandermeers-Piret M.C., Vanderm Robberecht P., Vandermeers Piret M.C., Vanderm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                        SEQUENCE
                                                                                                                                                                       -i- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY. PIR; C60415; C60415.
InterPro, I PRO00532, Glucagon.
Pfam; PF00123; hormone2; 1.
PRINTS; PR00275; GLUCAGON.
                                                                                                                                                                                                                                                   Peptides 11:123-128(1990).
-i- FUNCTION: STIMULATES FORMATION OF NAHCO(3)-RICH PANCREATIC JUICE AND SECRETION OF NAHCO(3)-RICH BILE AND INHIBITS HCL PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB001065; AAB90673.1; -.
TIGR; AF0569; -.
Hypothetical protein; Complete
SEQUENCE 60 AA; 7054 MW; B0
                                                                                                                       Glucagon family; Hormone; Amidation MOD_RES 27 27 AMIDAT
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01-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECR_RABIT
                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Small intestine;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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RLRDR
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(Rel.
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27, Last seq
32, Last ann
                                                                                                         3105 MW;
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54 MW; B62833AD3A00788B
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annotation update)
                                                               Score 15; DB 1;
Pred. No. 4.1e+02;
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Pred. No. 4.8e+02;
                                                                                                         38A015800BDD3618 CRC64;
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                                                                            Length 27;
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                                                                                                                                                                                                                                                                                                   "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90362066; PubMed=2167933;
Nicolson L., Cullinane A.A., Onions D.E.;
"The nucleotide sequence of an equine herpesvirus 4 gene homologue of the herpes simplex virus 1 glycoprotein H gene.";
J. Gen. Virol. 71:1793-1800(1990).
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL21,
EHV-1 40, EHV-4 UL21, AND VZV 38.
                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; No. Maite O., Clayton R.A., Kirkness B.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKerlavage A.R., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Equine herpesvirus type 4 (strain 1942) (EHV-4) (Equine herpesvirus type 1 subtype 2). Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus.
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
15-TW hypothetical protein HII507 in Mu-like prophage FluMu region.
HII507.
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                                                                               Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
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Pred. No. 5.8e+02;
1; Mismatches 1; Indels
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01-MAR-1992 (Rel. 21, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
Protein UL21 homolog (Fragment).
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Best Local Similarity 60.0%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U32827; AAC23166.1; -.
                                                                                                                                                                                                                                                                                                                              Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                   Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                           NCBI_TaxID=727;
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7 QLTER 11
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=92310993; PubMed=1614875;
Denny P., Swift S., Brand N., Dabhade N., Barton P., Ashworth A.;
"A conserved family of genes related to the testis determining gene, RRY.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Pred. No. 8.4e+02;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                         48.4%; Score 15; DB 1; Length 41; 40.0%; Pred. No. 6.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP, Q05066, JHRY.
InterPro, IPR00910, HMG 12_box.
Pfam, PF00505; HMG box, 1.
SMART, SM00398, HMG; 1.
DNA-binding, Nuclear protein, Transcription regulation.
                                                                                                                                                                                                                                                                                                                SEQUENCE 41 AA; 4683 MW; 341D6EE97859349F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 AA; 6536 MW; E08AlBFC00B3EDD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 20:2887-2887 (1992).
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: CONTAINS 1 HMG BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription factor SOX-5 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog)
                                                                                                                                                                                EMBL; D14486; BAA03380.1; -.
InterPro; IPR004936; Herpes_UL21.
Pfam; PF03252; UL21; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X65653; CAA46604.1; -. PIR; S21492; S21492.
PIR; S22949; S22949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopodinae, Xenopus
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YXXXXRLXER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YXXXXRLXER 10
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METJA

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Matches
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Q57966;
Q1-NOV-1997
Q1-NOV-1997
                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
21-JUL-1986 (Rel. 01, Last annotation update)
41-JUL-1986 (Rel. 01, Last annotation update)
421-JUL-1986 (Rel. 01, Last annotation update)
421-JUL-1986 (Rel. 01, Last annotation update)
422-JUL-1986 (Rel. 01, Last annotation update)
423-JUL-1986 (Rel. 01, Last sequence update)
423-JUL-1986 (Rel. 01, Last
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P03939;
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SEQUENCE
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MEDLINE=6337999; PubMed=688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                         STRAIN=cv. Tendergreen;
MEDLINE=85008540; PubMed=6090563;
                                                                                 SEQUENCE FROM N.A.
                                                                                                                                 NCBI_TaxID=3885;
                                                                                                                                                                                                                                                                                                                                                                                                                                         PHAVU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; MJ0546; -.
Hypothetical protein; Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U67504; AAB98548.1; -.
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3; Conserv
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
1 protein MJ0546.
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                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6460 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15; DB 1;
Pred. No. 8.7e+02;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLU-RICH.
66CBFC395548BA5D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                             58
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В
                                         Query Match
Best Local S
Matches 3
                                                                                                     transcript.";
J. Mol. Appl. Genet. 2:447-453(1984)
PIR; A04525; QQFB.
                                                                                    Hypothetical SEQUENCE 58
                                                                                                                                          "Structure of a chromosomal Phaseolus vulgaris lectin gene and its
48
                    6 RLXER 10
RLIQR 52
                                         3; Conserv
                                                                                    11 protein.
58 AA; 6859 MW;
                                          Conservative
                                                  48.4%;
                                         Score 15; DB
Pred. No. 9e+C
1; Mismatches
                                                                                     DA6BF0F01DB67D5E
                                                   DB 1;
9e+02;
                                                                                    CRC64;
                                                              Length 58;
                                          Indels
                                         0
                                         Gaps
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Search completed: December 19, 2002, 16:19:44
Job time: 5.55882 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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model
3
using
search,
protein
1
OM protein

December 19, 2002, 16:16:02; Search time 8.67647 Seconds (without alignments) 110.799 Million cell updates/sec Run on:

US-08-653-294C-39 Perfect score:

1 YXXXXRLXER 10 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

15911 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 60

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	, Length	DB	αι	Description
1	23	74.2	56	7	B89903	hypothetical prote
7	19	61.3	24	7	T42257	in ph
m	19	61.3	53	7	E97458	hypothetical prote
4	19	61.3	53	7	AG2676	
ហ	19	61.3	99	~	A69538	Ω
v	19	61.3	28	N	AB1589	hypothetical prote
7	19	61.3	28	N	A11650	hypothetical prote
80		58.1	47	7	JC5557	u
6		58.1	48	~	A84247	hypothetical prote
10		58.1	48	~	T01745	_
11	18	58.1	4.8	7	T01702	hypothetical prote
12		58.1	58	~	\$66328	8
13	18	58.1	59	7	E84008	hypothetical prote
14	17	54.8	~	N	T42259	
15	17		3	~	C87422	hypothetical prote
16	17	•	m	~	G97623	
17	17	٠	4	N	A61600	ď
18	17	54.8	2	7	T00166	hypothetical prote
19	17	٠	ß	~	866323	protein kinase AKI
	17		S	0	S77801	probable 6-phospho
21	16	51.6	7	0	A05296	fibrinogen alpha c
22	16		e	~	S25666	phosphopyruvate hy
23	16	•	4	7	S23641	
24	16	•	4	~	A83760	hypothetical prote
25	16	ä	S	4	870252	
26	16	•	2	N	S00991	_
27	16	٠	Ŋ	~	A83286	hypothetical prote
28	16	51.6	S	N	566324	Ω.
29	16	51.6	57	~	D90828	hypothetical prote

hypothetical prote hypothetical prote DR-beta chain MFC	hypothetical prote hypothetical prote probable endopepti	pimeloyl-CoA synth probable trypsin i protein kinase C i	protein kinase C i homeodomain protei transcobalamin - b	secretin - rabbit homeobox protein -	phycobilisome beta hypothetical prote
D82505 T12913 A69321	D85758 S49547 PC2371	A56786 S50741 S78575	S78574 S60564 S62672	C60415 I49747	F60691 F69827
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6 9 9 6 9 9	60 12 13	15 · 20 21	21 23 26	27	35
51.6 51.6 51.6	51.6 48.4 48.4	484 48.4 4.4.4	484 48.4 48.4	48.4	48.4
16 16 16	16 15	15 15 15	15 15	15 15	15
30 31 32	33 35 35	36 37 38	39 410	4 4 8 3	4 4 5

# ALIGNMENTS

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hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Obate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: B89903
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu:
Ma, A.; Miautani-Ui, Y; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Recession: B89903
A;Recession: B89903
A;Recence number: GB:BA000018; PID:g13701087; PIDN:BAB42382.1; GSPDB:GN00149
A;Cross-references: GB:BA000018; PID:g13701087; PIDN:BAB42382.1; GSPDB:GN00149
C;Genetics:
A;Gene: SAS037
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Gaps .; 0 74.2%; Score 23; DB 2; Length 56; 50.0%; Pred. No. 9; ive 0; Mismatches 5; Indels Query Match 74.2 Best Local Similarity 50.0 Matches 5; Conservative

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1 YXXXXRLXER 10 g à

21 YINAYRLAER 30

phosphoprotein phosphatase (BC 3.1.3.16) - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Oa.Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 02-Jun-2000
C;Accession: T42257
R;Zeke, T.; Gergely, P.; Dombradi, V.
R;Reference number: Z2231
A;Reference number: Z2231
A;Reference number: Z2231
A;Reference number: Z2237
A;Reference numb

ö Gaps . 0 Query Match
61.3%; Score 19; DB 2; Length 24;
Best Local Similarity 40.0%; Pred. No. 57;
Matches 4; Conservative 1; Mismatches 5; Indels

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C:Accession: C:Accession: R;Goodner, B.; Hinkle, G.; Gattung, O., R;Goodner, B.; Wollam, C.; Allinger, M.; Doughty, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen A;Title: Genome Sequence of the Plant Pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision C;Accession: A69538
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                                                                         A69538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: The Genome of the Natural Genetic A; Reference number: AB2577; PMID:11743193 A; Accession: AG2676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: AGR C 1494
A;Map position: ci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein AGR_C_1494 [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens
                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                A;Map position: circular
                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:
A;Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Authors: Yoo, H.;
ster, E.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein Atu0815 [imported] - Agrobacterium tumefaciens (strain C58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE007869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-53 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: E97458
                                                                                                                                                                                                                                                                                                                                                                                                                1;Residues: 1-53 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002;Accession: AG2676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 Accession: E97458
                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                        Genetics:
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                                                                                                                                                                                             RLXER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary
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                                                                                                                                                                                                                                                                                                                                                                         :AE008688; PIDN:AAL41829.1; strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G.; Gattung, S.; Miller, C.; Allinger, M.; Doughty,
                                                                                                                                                                                                                                                                                                                  chromosome
                                                                                                                                                                                                                                                    61.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.3%;
                                                                                                                                                                                                                                  Score 19; DB:
Pred. No. 1.3e.
0; Mismatches
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Pred. No. 1.3e
0; Mismatches
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                    05-Dec-1997
                                                           Archaeoglobus fulgidus
                                                                                                                                                                                                                              DB 2; L.
1.3e+02;
1;
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, D.; Scott, C.; Lappas, C.;
                                                                                                                                                                                                                                                                                                                                                                                           PID:g17739187;
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                  #text_change 22-Oct-1999
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Markelz, B.
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                                                                     Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                           R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baque:
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget,
                                                                                                                                                                                                                                C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision
C;Accessin: AII650
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                                    A;Status: preliminary
                                                           A; Accession: AI1650
                                                                                                                                                                             D.; Jones,
                                                                                                                                                                                                                                                                           hypothetical protein lin1746 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
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L.M.; Karst,

27-Nov-2001

#text\_change 27-Nov-2001

Baquero, F surget, O.;

F.; Berch; Entian,

Berche, P. tian, K.D.;

P.:

; Bloecker Fsihi, H.

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Waitournam, Voss, H.; W

m, A.; Ma Wehland,

<GLA>

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Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.I. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: A69538
                                                                                                                                                                                                                                                                                                                                                                                 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. A;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein lin1251 [imported] - Listeria innocua (strain Clip11262) C;Species: Listeria innocua (c;Species: Listeria innocua (c;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: AB1589
                                                                                                                                                                                                                                           A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                     A; Cross-references:
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                                                                                                                                                                                                                                                                                                                           A; Molecule type:
                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                A; Accession: AB1589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE000945; GB:AE000782; NID:g2689268; PIDN:AAB88955.1; PID:g264821
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A; Residues: 1-56 < KLE>
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RESULT 7
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                                                                                                                                                             Local Similarity
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                                                          RLSER
                                                                                                  RLXER 10
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                                                                                                                                                                                                                                                                                                                             DNA
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                                                                                                                                                                                                                                                              GB:AL592022; PIDN:CAC96482.1; ce: strain Clip11262
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Pred. No.
                                                                                                                                                           Score 19; DB 2;
Pred. No. 1.4e+02;
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J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness,
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                                                                                                                                                                                                                                                                                 PID:g16413725;
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Voss, H.; W
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Fsihi, H.
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: Wehland,
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hypotherical protein 48 - maize mitochondrion (fragment)
Cispecies: mitochondrion Zea may8 (maize)
Cispecies: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 29-Oct-1999
Ciscession: T01702
Rizheng, D.; Nielsen, B.L.; Daniell, H.
A; Title: A 7.5-kbp region of the maize (T cytoplasm) mitochondrial genome contains a ch)
A; Reference number: Z14403; MUID:97439744; PMID:9294260
A; Ascession: T01702
A; Ascession: T01702
A; Molecule type: DNA
                                                                                                                                          of chloroplast origin is
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 24-Sep-1999
C;Accession: 866328; 858263
R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A;Title: Differential accumulation of the transcripts of 22 novel protein kinase genes A;Reference number: 866314; MUID:9612333; PMID:8534852
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A;Experimental source: strain cmsT
                      Cipate: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 29-Oct-1999 CjAccession: T01745
Rizheng, D.; Daniell, H.
Rizheng, D.; Daniell, H.
Rizheng, D.; Daniell, H.
A;Description: Identification of tRNAIle (CAT), orf31 and orf48 of chloropla A;Reference number: 214415
A;Reference number: Z14415
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-48 <ZHE>
                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U18301; NID:g664761; PIDN:AAA83741.1; PID:g664762
C;Genetics:
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A;Residues: 1-58 <THU>
A;Cross_references: EMBL:X86960; NID:g928895; PIDN:CAA60523.1; PID:g928896
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Pred. No. 2.3e+02;
0; Mismatches 1;
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Pred. No. 2.3e+02;
0; Mismatches 1;
        C; Species: mitochondrion Zea mays (maize)
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80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
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A,Genome: mitochondrion
C,Keywords: mitochondrion
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Best Local Similarity
Matches 4; Conserv
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T01702
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R; Kimura, M.; Park, S.S.; Sakai, R.; Yamasaki, N.; Funatsu, G.
B; Kimura, M.; Park, S.S.; Sakai, R.; Yamasaki, N.; Funatsu, G.
B; Kimura, M.; Park, S.S.; Sakai, R.; Yamasaki, N.; Funatsu, G.
B; Sabosci. Biochem. 61, 984-988, 1997
A; Title: Primary structure of 6.5k-arginine/glutamate-rich polypeptide from the seeds of A; Reference number: JC5557, MUID:97357433; PMID:9214759
A; Accession: JC5557
A; Accession: JC5557
A; A; Residues: I-77 «KIM»
A; Residues: I-77 «KIM»
A; Residues: I-77 «KIM»
A; Experimental source: seed
C; Comment: This protein is a storage protein which provides nitrogen and carbon reserves F; I2-33, 16-29/Disulfide bonds: #status predicted
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R;NG; W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Danniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
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A;Cross-references: GB:AL592022; PIDN:CAC96977.1; PID:g16414233; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
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A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-48 <STO>
A;Cross-references: GB:AE004437; NID:g10580467; PIDN:AAG19341.1; GSPDB:GN00138
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                     arginine/glutamate-rich 6.5K polypeptide - smooth loofah
C;Species: Luffa cylindrica (smooth loofah)
C;Date: (2-Sep_1997 #sequence_revision 05-Sep-1997 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein Vng0907h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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Pred. No. 2.3e+02;
0; Mismatches 1; Indels
                                                                                                                                          Length 58
                                                                                                                                                                                          1; Indels
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Pred. No. 1.4e+02;
0; Mismatches 1;
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Pred. No. 2.3e+02;
0; Mismatches 1;
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T01745
hypothetical protein 48 - maize mitochondrion
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                                                                                                                                    Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
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ilarity 80.0%;
Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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                                                                               A,Gene: lin1746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain - Caenorhabditis elegans (fra
C;Species: Caenorhabditis elegans
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hypothetical protein CC1394 [imported] - Caulobacter crescentus C_iSpecies: Caulobacter crescentus
                                          C87422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: BH2869
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A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11558132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein BH2869 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: E84008
                                                             RESULT 15
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A;Residues: 1-59 <STO>
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                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z77733; PIDN:CAB01292.1
                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-24 < ZEK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Reference number: Z22131
                                                                                                                                                                                                                                                                                       Superfamily: phosphoprotein phosphatase; phosphoesterase core homology; phosphoproteir;
Keywords: phosphoric monoester hydrolase
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Ic subunits of Ser/Thr protein phosphatases from Caenorhabdit:
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Pred. No. 2.8e+02;
0; Mismatches 1
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Pred. No.
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Mismatches 5;
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C;Accession: C87422

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. R;Nierman, W.C.; Feldblyum, T.V.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, N.J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.
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A;Gene: CC1394
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A; Residues: 1-39 <STO>
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A, Accession: C87422
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C;Accession: C87422
                                                                                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                            Matches
                                                                                                                 Query Match
Best Local Similarity
27 RLCER 31
                                             6 RLXER 10
                                                                                            Conservative
                                                                                                                                                                                                                                  GB:AE005673; NID:g13422751; PIDN:AAK23375.1; GSPDB:GN00148
                                                                                                                   54.8%;
80.0%;
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                                                                                                                   Score 17; DB 2; Length 39; Pred. No. 3.7e+02;
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Search completed: December 19, 2002, 16:22:58 Job time: 9.67647 secs

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HLA-B2702.75-84(T)
HLA-B2702 CTL modu
Peptide B2702.75-8
Human Class I HLA-
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55.932 Million cell updates/sec
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| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA20000.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
                                                                                                                        Search time 23.8235 Seconds
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                            908470 seqs, 133250620 residues
                                                                                                                      December 19, 2002, 16:02:26;
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Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
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AAB59441
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31
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seq length: 60
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                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB
Maximum DB
                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                Searched:
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                                                                                                                        Run
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Gene #26 associate Arabidopsis thalia Peptide fragment o Peptide fragment o Peptide fragment o Alphal-helix of HLA-B2705.75-84. HLA-B2702.75-84(D) HLA-B2702.75-84(D) HLA-B2702.75-84 EPEPTIGE B2702.75-8 Peptide BANDOMULATORY PERIOD B2702.75-8 PEPTIDE B2702.75-8
                                                                                                                                                                                                                                                                                                Human Class I HLA-
HLA-B2702 CTL modu
Peptide B2702.70-8
HLA-B2702 CTL modu
Peptide B2702.84-7
Peptide B2702.84-7
                                                                                                                                                                                                                                                                            Immunosuppressive
Immunosuppressive
AAR92910
AAW33792
AAW33792
AAB65129
AAG66893
AAG1208
AAR41208
AAR41209
AAR41209
AAR86413
AAR896413
AAR83645
AAR83059
                                                                                                                                                                    AAW07513
AAW07515
AAW33784
AAW33786
AAW33786
AAW33796
AAW47265
AAW47269
AAY72487
AAY72487
AAY72487
AAY72487
AAY72487
                                                                                                                                                                                                                                                                                                                               AAB59415
AAB59455
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### ALIGNMENTS

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HIA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
                                                                                                                                                                        6
/note= "I6T mutation"
                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                (STRD ) UNIV LELAND STANFORD JUNIOR
                 AAR95426 standard; peptide; 10 AA
                                                                                                                                                                                                                                          94WO-US12985
                                                                                                                                                                                                                                                             93US-0150493
                                                       12-NOV-1996 (first entry)
                                                                          HLA-B2702.75-84 (T)
                                                                                                                                                              Key
Misc-difference
                                                                                                                                                                                                                                          10-NOV-1994;
                                                                                                                                                                                                                                                             10-NOV-1993;
                                                                                                                                                                                                     WO9513288-A1
                                                                                                                                                                                                                       18-MAY-1995
                                                                                                                                             Synthetic
                                     AAR95426;
       RESULT
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Clayberger C, Krensky AM,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see AAR95416), induces calcium influx, and inhibits cytotoxic Tlymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in acellular composition containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR95413, and AAR95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the HLA-B2702.75-84(T). These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide.
                 host
                             Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                 05-APR-1994;
                                                                                                                                                                                                                  05-APR-1995;
                                                                                                                                                                                                                                                   12-OCT-1995.
                                                                                                                                                                                                                                                                                    WO9526979-A1
                                                                                                                                                                                                                                                                                                                                                                                Cytotoxic T lymphocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                     HLA-B2702
                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR83095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR83095 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compsns. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-194027/25
                                                                                                                                                (STRD ) UNIV
                                                                                                                                                                                                                                                                                                                                                  immunosuppressant;
class I MHC; HLA-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L
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                                                                                 1995-358582/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REXLRXXXXXY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RENLRTALRY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                      CIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                 Lymphocyte; CTL; major histocompatibility complex; MHC;
ssant; graft versus host disorder; transplantation; therapy;
HLA-B2702.
                                                                                                                                                   LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                 modulating peptide (B2702.75-84(T)).
                                                                                                                  Krensky
                                                                                                                                                                                 94US-0222851
                                                                                                                                                                                                                  95WO-US04349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.2%;
50.0%;
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                                                                                                                  Parham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 23; DB Pred. No. 11; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
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Query Match
Best Local Similarity
Watches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunomodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84= a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR83061-R83085, AAR83090-R83096 and AAR92907-R92913 represent fragments of class I major histocompatibility complex (MHC), antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. This sequence showed no inhibitory effect upon cytotoxic T lymphocytes (CTLs). These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched domor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the CTLs of the
                                                                                                                                                                                                                    New immunomodulating alpha-1 domain, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW33788 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                       Peptides AAW33784-98 and AAW33778-9 were assayed for their
                                                                                                                                                                                                                                                                                                                                                               24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                              22-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                             27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9744351-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunomodulating transplantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide B2702.75-84T80 tested for immunomodulating activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW33788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 14; Page 34; 80pp; English
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                                                                                                                                                                                                                                                                                                                              UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                      1; Page 19; 41pp; English.
                                                                                                                                                                                                                                                                                             Clayberger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                               96US-0653294.
                                                                                                                                                                                                                                                                                                                                                                                              97WO-US08689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dimer; immunosuppressant drug; CTL activation;
autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                  diseases
                                                                                                                                                                                                                dimer peptide(s) -
for preventing reje
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.2%;
50.0%;
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                                                                                                                                                                                                                  s) - basedrejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                  on a Class I HLA-B of transplants or
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peptide type bond within the brackets.

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50.0%;

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         (positions
amino acid sequences related to a Class I HLA-B alphal domain (position 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibiting activation of cytotoxic T lymphocytes and/or natural killer cells involves combining cells with compound comprising oligopeptide with contiguous sequence of human leukocyte antigen-B alphal domain -
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; human leukocyte antigen-B; HLA-B; immunosuppressive;
cytotoxic T cell activation inhibition; cell transplantation;
natural killer cell activation inhibition; organ transplantation.
                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                       DB 19; Length 10;
                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Class I HLA-B alphal-domain-derived peptide #5.
                                                                                                                                                                                                                     74.2%; Score 23; DB 50.0%; Pred. No. 11; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Column 7-8; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       AAB59405 standard; Peptide; 14 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-0433613.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                        Local Similarity 50.0 tes 5; Conservative
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                                                                                                                                                                                                                                                                                             1 REXLRXXXXY 10
                                                                                                                                                                                                                                                                                                                           1 RENLRTALRY 10
                                                                                                                                                                                      10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB59405;
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                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                     Query Match
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Matches
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74.2%; Score 23; DB 22; Length 14;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a peptide which may be used in a method for inhibiting activation of cytotoxic T lymphocytes and/or natural killer cells. The method involves combining the cells with a compound comprising an oligopeptide of at least 6 amino acids comprising a contiguous sequence of a human leukocyte antigen (HLA)-B alphal domain including amino acids 84-86 åre YYW. The method is useful for transplanting a donor mammalian organ or cells to a mammalian recipient. The organ or cells are combined with the compound prior to implanting in the mammalian recipient, or the compound may be administered to the mammalian recipient, or the compound from prior to implanting the donor organ or cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibiting activation of cytotoxic T lymphocytes and/or natural killer cells involves combining cells with compound comprising oligopeptide with contiguous sequence of human leukocyte antigen-B alphal domain -
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                         Human, human leukocyte antigen-B; HLA-B; immunosuppressive; cytotoxic T cell activation inhibition; cell transplantation; natural killer cell activation inhibition; organ transplantation.
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                   Indels
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                                                                                                                                                                                                                                Human Class I HLA-B alphal-domain-derived peptide #10.
                 5
    Pred. No. 16;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                              AAB59410 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB59436 standard; Peptide; 14 AA.
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                                                                                                                                                                                                     (first entry)
                5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-111720/12.
Best Local Similarity
Matches 5; Conserv
                                            1 REXLRXXXXY 10
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                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                         AAB59410;
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                                                                                                                  RESULT 5
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RESULT 7
AAB59439
ID AAB5
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   US6162434-A
                            Synthetic
                                           Homo sapiens
                                                                      cytotoxic T ce
natural killer
                                                                                    Human; human leukocyte antigen-B; HLA-B; immunosuppressive; cytotoxic T cell activation inhibition; cell transplantation;
                                                                                                                               Human Class I HLA-B alphal-domain-derived peptide #39.
                                                                                                                                                            22-MAR-2001
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                                                                                                                                                                                                                   AAB59439 standard; Peptide;
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                                                                        activation inhibition;
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The method is useful for transplanting a donor mammalian organ or cells to a mammalian recipient. The organ or cells are combined with the compound prior to implanting in the mammalian recipient, or the compound may be administered to the mammalian recipient in a period extending from prior to implanting the donor organ or cells.
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                                      Buelow
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WPI; 2001-111720/12.

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                                                                                                                           inhibiting activation of cytotoxic T lymphocytes and/or natural killer cells. The method involves combining the cells with a compound comprising an oligopeptide of at least 6 amino acids comprising a contiguous sequence of a human leukcoyte antigen (HiA) B alphal domain including amino acids 84-86, where amino acids 84-86 are YYW. The method is useful for transplanting a donor mammalian organ or cells to a mammalian recipient. The organ or cells are combined with the compound prior to implanting in the mammalian recipient, or the compound may be administered to the mammalian recipient in a period extending
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Inhibiting activation of cytotoxic T lymphocytes and/or natural killer cells involves combining cells with compound comprising oligopeptide with contiguous sequence of human leukocyte antigen-B alphal domain -
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cytotoxic T cell activation inhibition; cell transplantation;
natural killer cell activation inhibition; organ transplantation.
                                                                                                                sequence is a peptide which may be used in a method
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to a mammalian recipient. The organ or cells are combined with the compound prior to implanting in the mammalian recipient, or the compound may be administered to the mammalian recipient in a period extending from prior to implanting the donor organ or cells.
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Pred. No. 16;
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                                                                                                                                                                                                                                                                          AAR92909 standard; peptide; 20 AA.
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50.0%;
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Matches 5; Conserv
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Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                       Peptide
                                                                   19-JUN-1998
                                                                                               AAW33792
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                                                                                                                                                                                                                                                                                                   Sequence
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                                        B2702.84-75/75-84T tested for immunomodulating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR83090-R83096 and AAR92907-R92913 represent translaw (MHC) antiqens. This
                                                                                                                                                                                                                                                           74.2%;
                                                                                                                                                                                                                                               Score 23; DB Pred. No. 22; 0; Mismatches
                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parham P;
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                                                                                                                                                                                                                                                        DB
22;
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                                        activity
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RESULT 13
AAW33793
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                              AAW33793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunomodulating activity. A peptide-type compound or variant is claime which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                             rejection.
                                                                                                                                              transplantation;
                                                                                                                                                                     Immunomodulating
                                                                                                                                                                                                                           Peptide B2702.84-75T/75-84T tested for immunomodulating activity.
                                                                                                                                                                                                                                                                                         19-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                         AAW33793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 19; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treating autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New immunomodulating alpha-1 domain, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-086530/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beulow R, Clayberger C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptides AAW33784-98 and AAW33778-9 were assayed for their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-NOV-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       μ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REXLRXXXXXY 10
                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0653294.
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                                                                                                                                        dimer; immunosuppressant drug; CTL activation;
autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                      peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dimer peptide(s) - based for preventing rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Krensky AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
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transplants
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Homo sapiens

Synthetic.

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07-JUN-1999;
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23-MAR-1999;
25-MAR-1999;
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23-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG06983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                              healing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                             Peptides AAW33784-98 and AAW33778-9 were assayed for their immunomodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = CC R aa76-71) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = CC R aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and ar represents amino acid requence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection or treating autoimmune diseases, e.g. diabetes, constant also be constant and lupus erythematosis. The products can also be constant and and lupus erythematosis. The products can also be constant and constant
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                                                                                                                                                                                                                       New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secreted protein; gene therapy; vaccine; cancer; leukemia; autoimmune disease; allergy; inflammation; graft rejection; hyperproliferation; cardiovascular; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 74.2%; Score 23; DB 19; Length 20; Best Local Similarity 50.0%; Pred. No. 22; Matches 5; Conservative 0; Mismatches 5; Indels
                                                                                                                                                         Beulow R, Clayberger C, Krensky AM,
                                                                                                                           (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                       Example 1; Page 19; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB65129 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene #26 associated peptide #20.
                                                                                             96US-0653294.
                                                             97WO-US08689
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                                                                                                                                                                                         WPI; 1998-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 REXLRXXXXX 10
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                                                            22-MAY-1997;
WO9744351-A1
                                                                                             24-MAY-1996;
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                              27-NOV-1997
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                          Nucleic acids encoding 26 human secreted polypeptides, useful e.g. for preventing, diagnosing and/or treating cancers and for promoting wound
                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to 26 secreted human proteins. The proteins may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. For example, they may be used in gene therapy or in vaccines. Typical of diseases which are potentially treatable are cancers (including leukemia), autoimmune diseases, allergies, inflammation, graft rejection, hyperproliferation, cardiovascular diseases (particularly critical limb ischemia and coronary disease) involving abnormal anglogenesis, neurodegeneration and/or
                                                                                                         Shi Y;
Young PE;
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                                                                                                         Soppet DR, Rosen CA,
Florence KA, Ni J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 3960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 81; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG06983 standard; Protein; 44 AA.
                                                                                                   Duan RD, S.
, Ebner R,
                                                   (HUMA-) HUMAN GENOME SCI INC.
99US-0137725.
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                                                                                                      Ruben SM; Birse CE, D
Lafleur DW, Olsen HS,
                                                                                                                                                                                      WPI; 2001-061741/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infectious diseases.
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Matches 5, Conserv
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15-JUL- 16-JUL- 19-JUL- 19-JUL- 19-JUL- 19-JUL- 19-JUL- 19-JUL- 20-JUL- 20-JUL- 20-JUL- 20-JUL-	24-Jun 28-Jun 29-Jun 30-Jun 01-Jun 01-Jun 02-Jun 08-Jun 12-Jun 11-Jun	18-JUN- 22-JUN- 23-JUN- 23-JUN-	28-MAY 01-JUN 03-JUN 03-JUN 04-JUN 07-JUN 08-JUN 10-JUN 110-JUN	28-APR-19 30-APR-19 30-APR-19 04-MAY-19 05-MAY-19 06-MAY-19 06-MAY-19 06-MAY-19 11-MAY-19 11-MAY-19 14-MAY-19 14-MAY-19 14-MAY-19 14-MAY-19 21-MAY-19 21-MAY-19 21-MAY-19 21-MAY-19
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Search completed: December 19, 2002, 16:19:05 Job time : 23.8235 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

December 19, 2002, 16:14:32; Search time 17.6471 Seconds (without alignments)
116.760 Million cell updates/sec Run on:

US-08-653-294C-38

1 REXLRXXXXY 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 segs, 206047115 residues Searched:

45785 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 60

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL 21:\*
1: SP\_archea:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

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Odate)	annotation update)	Craniata, Vertebrata, Euteleostomi, Sciurognathi, Muridae, Murinae, Mus			Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda	Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T. Okazaki V. Golobori T. Rono H. Kasukawa T. Saito	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio	P., de Bona	ta M., Garib A Kamiva M	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Stor	Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming		a full-length mouse cDNA collection.";	
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111 1 110 29CUL0 99CUL0; 01-JUN-2001	01-MAR-2002 (TrEMBLrel. 20, Last 6530404A22Rik protein (Fragment).	ossovychzzkróm Mus musculus (Mouse). Bukaryota; Metazoa; Chordata; Mammalia; Butheria; Rodentia; NCBI TaxID=10090;	[1] SEQUENCE FROM N.A.	SIRAIN=C3/B1/80; IISSUB=IESIIS; MEDLINE=21085660; PubMed=11217851;	Kawai J., S.	Aizawa K.,	Kadota K., 1	Fleischmann Kuehl P., L	Schriml L.M	Blake J., B	Brownstein   Gustingich	Lyons P., M	Nordone P.,	Suzuki H.,	Hayashizaki Y.;	"Functional annotation of Nature 409:685-690(2001)	EMBL; AK015634; BAB29909.1; MGD; MGI:1915046; 6530404A22Rik.
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Submitted (JUN-1997) to the EN

EMBL; AF011546; AAD46382.2; -

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PROSITE; PS00294; PRENYLATIO
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SEQUENCE 52 AA; 5506 MW;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HLA-B27 variant exon 2 (Alphal domain) (Fragment).
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                                                                     CRC64;
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   Length 48;
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                                       Query Match
Best Local S
Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Adams B., McLean I.L., Robert
Submitted (JUN-1997) to the E
EMBL, AF011549; AAD46385.2; -
InterPro; IPR001039; MHC_I.
Pfam; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996
01-NOV-1996
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000
01-DEC-2001
MHC class I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9TQC2;
Q9TQC2;
01-MAY-2000
                                                                                                                                                    FlyBase;
                                                                                                                                                                                                                                                                                                                                                                        Drosophila pseudoobscura (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER
                                                                                                                              SEQUENCE
                                                                                                                                                                                                           "Nucleotide sequence of the Xdh region in I an analysis of the evolution of synonymous Mol. Biol. Evol. 6:33-52(1989).
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=89158785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L(3)87DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LETHAL(3)87DF protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q24623;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLA-B.
                                                                                                                                                                                         EMBL; M33977; AAA29021.1;
                                                                                                                                                                                                                                                                          Riley M.A.;
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7237;
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REXLRXXXXX 10
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                                         Similarity
4; Conserv
                                                                                                                                                                   FBgn0012726;
                                                                                                                            51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TTEMBLrel. 13, Created)
(TTEMBLrel. 13, Last sequence update)
(TTEMBLrel. 19, Last annotation update)
HLA-B (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                PubMed=2493563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5841 MW;
                                                                                                                            6212 MW;
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50.0%;
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                                                             67.7%;
40.0%;
                                                                                                                                                                   Dpse\1(3)87Df.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                         Score 21; DB 5;
Pred. No. 1.4e+02;
1; Mismatches 5
                                                                                                                            C5023140B744A005 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                region in Drosophila pseudoobscura
synonymous codons.";
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Mismatches
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                                           Indels
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PSEQUENCE FROM N.A.

RADILINE=21595285; PubMed=11759840;
RA MEDLINE=21595285; PubMed=11759840;
RA Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Matazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
"Complete genomic sequence of the filamentous nitrogen-fixing
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT Cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).

EMBL; AP0015597; BAB76339.1; -.

EMBL; AP0015597; BAB76339.1; -.

KW Hypothetical protein; Complete proteome.

SEQUENCE 57 AA; 6401 MW; 2F552487C9BC7CD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein As14640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                            PRELIMINARY;
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   || ||
41 RESLR 45
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                                                                                                                         RESULT 8
10 08 YNC
AC 08 YN
DT 01-M
DT 01-M
DT 01-M
DT 01-M
DT 01-M
DE HYPO
OC BACL
OC BACL
OC BACL
OC BACL
CON RA ABLA
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QBVYX6
DQ QBVX
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                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=BLOOD;
Arnaiz-Villena A., Martinez-Laso J., Gomez-Casado E., Bedoya C.,
Montoya P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Yoshida M., Kimura A., Katsuragi K., Numano F., Sasazuki T.;
"DNA typing of HLA-B gene in Takayasu's arteritis.";
Tissue Antigens 42:87-90(1993).
InterPro; IPR01039; MHC I.
Prodom; PP00129; MHC I.
Probom; P000050; MHC I; 1.
Probom; P000129; MHC I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19; DB 7; Length 46; Pred. No. 4.5e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 80.0%; Pred. No. 4.6e+02; 4; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "HLA-B new alleles in South American Indians.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER 1 1 1 NON_TER 47 47 87 SEQÜENCE 47 A2, 5608 MW; 30AF5787E6669B02 CRC64;
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NON_TER 46 46
SEQUENCE 46 AA; 5500 MW; 62ACB787E666D8F4 CRC64;
                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
MHC class I (Fragment).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HLA class I antigen (Fragment).
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                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 136980; AAL31360.1; —.
InterPro; IPR001039; MHC I.
Pfam; PF00129; MHC I; 1.
Probom; PD000050; MHC I; 1.
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80.0%;
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                                                                                                                                                                                         PRELIMINARY;
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
|| :| |
28 REAMRRQALY 37
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Q8WM99
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Gaps

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61.3%; Score 19; DB 16; Length 57; 80.0%; Pred. No. 5.5e+02; Live 0; Mismatches 1; Indels

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                                               O'VANAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Ultraviolet-B-inducible auxin-related protein (Fragment).
Pisum sativum (Garden pea).
Pisum sativum (Aridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I: Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
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                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Liu L., White M.J., MacRae T.H.;
"Identification of ultraviolet-B responsive genes in the pea, Pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.3%; Score 19; DB 10; Length 60;
80.0%; Pred. No. 5.8e+02;
tive 0; Mismatches 1; Indels
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY065659, AAL50319.1; -.
NON TER
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60 AA.
PRT;
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PRELIMINARY;
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RESULT 10

1 REXLR

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Q9QZX5
AC Q9QZX5;
AC Q9QZX5;
AC Q9QZX5;
DT 01-MAY--
DT 01-JUN--
DE Desmopla
GN DSP.
OS Mus mus
OC Eukaryol
OC Mammali
OX NCBITA
RP SEQUENCI
RC STRAIN=-
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RESULT 12
Q95SN4
ID Q95SN
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Q902X9
ID Q902X9
AC Q902X9
DT 01-W1
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DT 01-JI
DT 01-JI
DT 01-W2
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Best Local S
Matches 4
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01-MAY-2000
01-MAY-2000
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Green K.J., Guy S.G., Cserhalmi-Friedman P., McLean W.H.
Christiano A.M., Wagner R.M.;
"Analysis of the desmoplakin gene reveals striking conse
other members of the plakin family of cytolinkers.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF148515; AAF02528.1; -.
MCD; MGI:109611; Dsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus spretus (Western wild mouse).
Bukaryota; Metazoa; Chordata; Cra
Mammalia; Eutheria; Rodentia; Sci
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Green K.J., Guy S.G., Cserhalmi-Friedman P., McLean W.H.I.,
Green K.J., Guy S.G., Cserhalmi-Friedman P., McLean W.H.I.,
Christiano A.M., Wagner R.M.;
"Analysis of the desmoplakin gene reveals striking conservation with
"brief members of the plakin family of cytolinkers.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF148514; AAF02527.1; -
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Eukaryota; Metazoa;
Mammalia; Eutheria;
  Q95SN4
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01-JUN-2002
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Rodentia;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                             3B41DF23C1E2F960 CRC64;
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  PRT;
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Sciurognathi; Muridae;
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RESULT 14
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Q83274
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01-DEC-2001
01-DEC-2001
01-MAR-2002
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STRAIN=743;

Masuta C., Hayashi Y., Wang W.Q., Takanami Y.;

Masuta C., Hayashi Y., Wang W.Q., Takanami Y.;

"Comparison of four satellite RNA isolates of of the comparison of four satellite RNA isolates of the comparison of four satellite RNA isolates of the comparison of the compariso
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01-NOV-1996
                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Genome polyprotein [Contains: envelope glycoprotein (NS1)] (Fragment).
                                                                                                                                                                                                                                              Q9J5W8;
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Q83274;
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EMBL, AV060509, AAL28238, 1, -
ENBL, AV060509, AAL28238, 1, -
ENBL, AV060509 aAL28238, 1, -
ENBL, E
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BEST:GH10831 OR CG8343.
BEST:GH10831 OR CG8343.
Drosophila melanogaster (Fruit fly).
Brosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cucumovirus.
NCBI_TaxID=12305;
Hepatitis C virus.
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80.0%;
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Last annotation updat
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Pred. No.
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Pred. No. 4e+02;
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4.9e+02;
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MEDLINE-20219428; PubMed=10756048;
MARTINE-20219428; PubMed=10756048;
MARTINE-20219428; PubMed=10756048;
MARTINE-A. Solforosi L., Debiaggi M., Zara F., Tanzi E., Romano L.,
Zanetti A.R., Clementi M.; Pebiaggi M., Zara F., Tanzi E., Romano L.,
T. "Dominant role of host selective pressure in driving hepatitis C virus
TY "Dominant role of host selective pressure in driving hepatitis C virus
TY 414327-4334(2000).

BMBL; AF192441; AAF65652.1; -.
REMBL; AF192441; AAF65652.1; -.
REMBL; AF192441; AAF65652.1; -.
Remai, PRO1560; HCV NS1.
Remai, PRO1560; HCV NS1.
Remai PRO1560; HCV NS1.
Remai PRO1560; HCV NS1.
TOWN_TER 1 1
TOWN_TER 27 27
SEQÜENCE 27 AA; 3053 MW; FC584F0131E665CF CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2000 (TrEMBLrel. 14, Last annotation update)
3.7 kDa napin-like protein small chain (Fragment).
Momordica charantia (Bitter gourd) (Balsam pear).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Pred. No. 5.1e+02;
2; Mismatches 5; Indels
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Biochim. Biophys. Acta 1298:223-240(1996).
SEQUENCE 30 AA; 3737 MW; 21B6BE02D63DECD9 CRC64;
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MEDLINE=97135090; PubMed=8980648;
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Best Local Similarity 30.0
Matches 3; Conservative
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7 REAVRHTTSF 16
                                                                                                                                                   SEQUENCE FROM N.A.
                                     Hepacivirus.
NCBI_TaxID=11103;
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Q9S871;
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1095871
AC 095871
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Search completed: December 19, 2002, 16:21:51 Job time : 18.6471 secs

13 REQLR 17

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GenCore version 5.1.3
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OM protein - protein search, using sw model

December 19, 2002, 16:16:02 ; Search time 8 67647 Seconds (without alignments) 110.799 Million cell updates/sec Run on:

US-08-653-294C-38

1 REXLRXXXXX 10 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

15911

Minimum DB seq length: 0 Maximum DB seq length: 60

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
1	21	67.7	51	. 2	B31946	hypothetical prote
7	19	61.3	35	N	D69330	prot
Э	19		57	7	AH2385	
4	19	61.3		N	801800	•
ഗ	18	58.1	33	~	B44906	Ļ
9	18	58.1	33	7	C97406	othetical
7	18	58.1		7	AH0844	
æ	18	58.1		7	156173	- 12
σ	18	58.1		~	S13571	hypothetical prote
10	18	58.1		7	G84198	
11	18	58.1		~	E81927	
12	18	58.1		4	JE0018	×
13	18	58.1		7	156605	17 alpha-hydroxyla
14	18	58.1		7	A69385	hypothetical prote
15	18	58.1		0	G84072	
16	18	58.1		7	B75147	lsu ribosomal prot
17	18	58.1		4	JA0077	×
18	17	54.8		~	B85928	
19	17	54.8		~	C47214	u
20	17	54.8		~	T29970	hypothetical prote
21	17	54.8		~	AB0724	conserved hypothet
22	17			N	B61510	translation_elonga
23	16	ä		~	T01691	hypothetical profe
24	16	•		N	A44906	ı
25	16	ä		N	S33646	hypothetical prote
. 56	16	Η.		N	G70236	_
27	16	51.6		~	A70106	_
28	16	51.6	46	~	84	Н
29	16	51.6	46	~	AH2518	Н

hypothetical prote hypothetical prote 50S ribosomal prot	hypothetical prote probable zinc fing hypothetical prote	hypothetical prote relaxin - spiny do ribosomal protein	ribosomal protein nef protein - huma hypothetical prote	hypothetical prote hypothetical prote	nyponnetical proce ribosomal protein
AG3362 C82773 E82981	S76541 S42357 F81545	AB2484 A26463 E82347	D64104 S07344 H95181	AD1819 AH2103	S50004
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9 9 7 9 9	16 16 16	16	16 16	9 9 4	16
330	3.3 3.4 5.4	36 38 38	39 440 11	4 4 4 2 8 4 4	45

### ALIGNMENTS

RESULT 1 B31946	
hypothetical protein (xdh 5' region) - fruit fly (Drosophila pseudoobscura) (fragment) C;Species: Drosophila pseudoobscura	ragment)
C;Date: 22-Nov-1989 #sequence revision 22-Nov-1989 #text change 20-Mar-1998	
C;Accession: B31946	
R;Riley, M.A.	
Mol. Biol. Evol. 6, 33-52, 1989	
A; Title: Nucleotide sequence of the Xdh region in Drosophila pseudoobscura and an analys	an analys
A;Reference number: A31946; MUID:89158785; PMID:2493563	
A;Accession: B31946	77
A. Ottobers	

A,Status: preliminary A,Molecule type: mRNA A,Residues::1-51 <RIL> A,Cross-references: GB:M33977; NID:g158807; PID:g158808

C,Genetics:

A,Gene: FlyBase:Dpse/ry A,Cross-references: FlyBase:FBgn0012736

Gaps ; Length 51; 5; Indels 7 Score 21; DB 2 Pred. No. 43; 1; Mismatches 67.78; Query Match
Best Local Similarity 40.0
Matches 4; Conservative

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1 REXLRXXXXY 10 à 셤

| | : | | 1 28 REAMRRQALY 37

hypothetical protein AF0644 - Archaeoglobus fulgidus
C;Species: Os-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999
C;Accession: D69330
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woses, C.R.; Venter, J.C.
A;Authors: Cmplete genome sequence of the hyperthermophilic, sulfate-reducing archaec A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA

A;Cross-references: GB:AE001060; GB:AE000782; NID:g2689383; PIDN:AAB90607.1; PID:g264998

ö Gaps ; 0 Query Match 61.3%; Score 19; DB 2; Length 35; Best Local Similarity 80.0%; Pred. No. 1.1e+02; Matches 4; Conservative 0; Mismatches 1; Indels

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L1 protein - human papillomavirus type Xd (fragment)
C;Species: human papillomavirus type Xd
C;Bate: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 26-Aug-1999
C;Accession: B44906
                 R;van den Brule, A.J.; Snijders, P.J.; Raaphorst, P.M.; Schrijnemakers, H.F.; Delius, H. J. Clin. Microbiol. 30, 1716-1721, 1920. Aprile: General primer polymerase chain reaction in combination with sequence analysis A;Reference number: A44889; MUID:92332706; PMID:1321168
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C; Keywords: aspartic proteinase; hydrolase; protein digestion
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C;Superfamil
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein A; Residues: 1-60 < TAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Tanji, M.; Kageyama, T.; Takahashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pepsin (EC 3.4.23.-) 3 precursor - North Pacific bluefin tuna (fragment)
C;Species: Thunnus thynnus orientalis (North Pacific bluefin tuna)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Nov-1
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2385
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A;Experimental source: strain PCC 7120
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A;Residues: 1-57 <KUR>
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Kaneko, T.; Nakamura,
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#text_change 30-Jun-2002
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th, T.; co..., O'Gaora, ...
Nature 413, 848-552, 2001
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A;Reference number: A97359; PMID:11743194
A;Accession: C97406
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                                                                                                                                                                                      A; Cross-references:
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A; Residues: 1-37 < PAR>
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A;Accession: AH0844
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A; Residues: 1-33 < KUR>
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A;Experimental source: type Xd, cerrical carcinoma in situr
A;Note: sequence extracted from NCBI backbone (NCBIN:109401, NCBIP:10945)
C;Superfamily: papillomavirus L1 protein
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A; Residues: 1-33 < VAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ıgan, G.; James,
P.; Cronin, A.;
                                                                                                                                                                                      GB:AL513382; PIDN:CAD05943.1; PID:g16503914;
                                58.1%;
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80.0%;
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Pred. No. 2e+02;
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Pred. No.
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   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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, P.; Davies, R.M.; Dowd,
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2e+02;
                             DB 2; 1
2.2e+02;
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Markelz,
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rkelz, B.;
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hypothetical protein NMA0824 [imported] - Neisseria meningitidis (strain 22491 serogroug C;Species: Neisseria meningitidis (C;Date: 05-May-2000 #text_change 02-Feb-2001 (C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 (C;Accession: E81927 (C;Accession: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84106.1; PID:g737954; Bxperimental source: serogroup A, strain Z2491
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JE0018
probable 6.1K protein pseudogene - cucumber mosaic virus (strain Indonesia, isolates X27 C;Species cucumber mosaic virus, CMV
C;Species cucumber mosaic virus, CMV
C;Date: 31-Dec-1991 #sequence_revision 28-May-1998 #text_change 20-Oct-2000
C;Accession: JE0018
R;Kaper, J.M.; Tousignant, M.E.; Steen, M.T.
R;Kaper, J.M.; Tousignant, M.E.; Steen, M.T.
A;Title: Cucumber mosaic virus-associated RNA 5. XI. Comparison of 14 CARNA 5 variants 1 A;Reference number: JE0018; MUID:88179532; PMID:3354198
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A;Residues: 1-54 «KAP»
A;Cross-references: GB:M20354; GB:M20355; NID:g331670; NID:g331674; PIDN:AAA46396.1; PII
                           A;Cross-references: GB:AE004437; NID:g10580015; PIDN:AAG18955.1; GSPDB:GN00138 C;Genetics:
A;Gene: VNG0402H
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A;Status: translation not shown; conceptual translation of pseudogene
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Pred. No. 3.3e+02;
0; Mismatches 1; Indels
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Pred. No. 3e+02;
0; Mismatches
                                                                                                                                                                                                                     DB 2;
3e+02;
                                                                                                                                                                                                                     Score 18; DB
Pred. No. 3e+0
0; Mismatches
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80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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A;Molecule type: DNA
A;Residues: 1-50 <PAR>
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C;Species: Halobacterium species NRC-1
C;Species: Halobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human Jurkat T cell line: evide
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R; Huang, D.C.; Novel, M.; Novel, G. FEMS Microbiol. Lett. 77, 101-106, 1991
A; Title: A transposon-like element on the lactose plasmid of Lactococcus lactis subsp. A; Reference number: S13568
                                                                                                                                                                                                                                                                                                                               Cibte: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_cnange 21-Jul-2000 Cibte: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_cnange 21-Jul-2000 Cibte: 02-Jul-1996 #setion: 156173
Risinha, S.K.; Todd, S.C.; Hedrick, J.A.; Speiser, C.L.; Lambris, J.D.; Tsoukas, C.D. J. Immunol. 150, 5311-5320, 1993
A;Title: Characterization of the EBV/C3d receptor on the human Jurkat T cell line: evi A;Reference number: 156173; MUID:93294286; PMID:8390533
A;Accession: 156173
A;Accession: 156173
A;Accession: 156173
A;Accession: 156173
A;Accession: 156173
A;Residues: 1-39 <RES>
A;Accession: RNA
A;Residues: 1-39 <RES>
A;Cross-references: GB:S62696; NID:g386263; PIDN:AAB27186.1; PID:g386264
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A;Experimental source: insertion sequence 1076; plasmid pUCL22; strain Z270
C;Genetics:
A;Mobile element: insertion sequence 1076
                                                                                                                                                                                                                                                                                                        Species: Homo sapiens (man)
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A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-48 <HUA>
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30 REVLR 34
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Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: A69385
A;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB07102.1; GSPDB:GN00 A;Experimental source: strain C-125 C;Genetics: A;Gene: BH3383
                                                                                                                                                                                                                     R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hix: Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                 hypothetical protein BH3383 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Deceies: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: G84072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein AF1081 - Archaeoglobus fulgidus (;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999 C;Accession: A69385
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C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: heme; transmembrane protein
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C;Date: 26-Jul-1996 #sequence_revision 26
C;Accession: I56605
                                                                                                            A; Molecule type: DNA
A; Residues: 1-57 <STO>
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A; Accession: G84072
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A;Molecule type: DNA
A;Residues: 1-56 <RES>
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,Residues: 1-57 <KLE>
,Cross-references: GB:AE001028; GB:AE000782; NID:g2689351; PIDN:AAB90166.1; PID:g264951
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Search completed: December 19, Job time: 9.67647 secs

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Hypothetical protein AF0644.
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              GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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seq length: 60
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Maximum DB
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=9049343, PubMed=9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Krypides N.C.,

Richardson D.L., Werlawsh J., Lee N.H., Sutton G.G., Gill S.,

Rirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Asdow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Nature 390:364-370(1997).
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Pred. No. 45;
0; Mismatches 1; Indels
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Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
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Hypothetical protein; Complete proteome.
SEQUENCE 35 AA; 4056 MW; 34FBE02042F10226 CRC64;
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Last annotation update)
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OSTC_LEPNA
OSTC_LEPNA
DIUH_ERAM
DIUH_ZOONE
LA89_LACAC
OSTC_XIPGL
RL34_MYCGE
YCX7_OENIO
PPLA_CHICK
YG65 HAEIN
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RESULT
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NON_TER
                                                                                                                                                                                                                                                                                                                    genome analysis program.";
Theor. Appl. Genet. 93:997-1005(1996).
                                                                                                                                                                                                                                                                                                                                                                           Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C., Pernollet J.-C., Zivy M., de Vienne D.; "The maize two dimensional gel protein database: towards an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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- I. SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.

PIR; S01800; S01800.

HSSP; P20142; 1HTR.

MEROPS; A01.001; -
   SEQUENCE
                                                                                                         Maize-2DPAGE;
MaizeDB; 12395
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01-OCT-1996 (Rel. 34, Last seg
15-JUL-1999 (Rel. 38, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UC27 MAIZE P80633;
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"Tuna pepsinogens and pepsins. Purification, characterization and amino-terminal sequences.",
Eur. J. Biochem. 177:251-259(1988).
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01-FEB-1991 (Rel. 17, Last sequence update)
15-UNV-2002 (Rel. 41, Last annotation update)
Pepsin 3 precursor (EC 3.4.23.-) (Fragment).
Thunnus thymnus orientalis (North Pacific bluefin tuna)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEP3_THUTO P20141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Coleoptile;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROPEP
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InterPro; IPR001969; Aspprotease_site.
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                                                                                                                                                                       OY. Appl. Genet. 93:997-1005(1996).
MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.4, ITS MM IS: 48.4 kDa.
SIMILARITY: TO XENOPUS HISTONE-BINDING PROTEIN N1/N2 AND RABBIT
AND HUMAN NUCLEAR AUTOANTIGENIC SPERM PROTEIN.
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   Α.
                                                                                                                                          P80633; COLEOPTILE.
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   1853
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2D-page of etiolated coleoptile (Spot 688)
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   MW;
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0; Mismatches
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Pred. No.
       CA0E12A5DAED8DC7 CRC64;
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RESULT 5
YA81_ARCFU
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TAC COORDINATE
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Best Local
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029182;
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16-OCT-2001
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SEQUENCE
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P41967;
               Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE NPY / PPY InterPro; IPR001955; Pancreatic_hormn. Pfam; PF00159; hormone3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maule A.G., Shaw Moore S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00265; PANCREATIC_HORMONE_1; PROSITE; PS50276; PANCREATIC_HORMONE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00309; PAH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parasitology 105:505-512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maule A.G., Shaw C., Halton D.W., Thim L., Johnston C.F., Fairweather I., Buchanan K.D.; Parawieren regulatory peptide from "Neuropeptide F: a novel parasitic flatworm regulatory peptide from Moniezia expansa (Cestoda: Cyclophyllidea).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Platyhelminthes;
Cyclophyllidea; Anoplocephalidae; Mor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moniezia expansa (Sheep tapeworm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neuropeptide F (NPF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995
                                                                                                      AF1081.
                                                                                                                       Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93096525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parasitology 102:309-316(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=28841;
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4; Conservative
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                                                                                                                     (Rel. 40, Created)
(Rel. 40, Last sequence
(Rel. 40, Last annotation
protein AF1081.
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                                                                                                                                                                                                                                STANDARD;
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32, Last
40, Last
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C., Halton D.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4594 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                      58.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18; DB
Pred. No. 95;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18;
Pred. No.
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2D61A76927DEA732
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                                                                                                                                                                   update)
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                                                            Archaeoglobales;
                                                                                                                                         update)
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                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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EMBL; M11204; AAA46676.1; -.
Nucleocapeid.
NON TER 42 42
SEQÜENCE 42 AA; 4917 MW;
                                                                                                                                        1 REXLRXXXXY 10
                                                                                                                                                                   26 ŘÉYĽQSRRPÝ 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella.
                                                                                                                                                                                                                                                 GNS SALTY
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                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                        MINITED 8049343; PubMed=3080475; Minite O., Nelson K.E., Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Klenk H.-P., Clayton R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Gatham D.E., Kyrpides N.C., Pleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.P., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., Morkeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Sadow P.W., D'Andrea K.P., Bowman C., Faine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELEMENT CONFERRING HELICAL SYMMETRY ON THE NUCLEOPROTEIN CORE AS WELL AS INTERACTING WITH M PROTEIN DURING VIRION FORMATION.
-!- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES NUCLEOCAPSID FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-85274370; PubMed-4024452;
Kurilla M.G., Stone H.O., Keene J.D.;
Kurilla M.G., Stone H.O., Keene J.D.;
Newcastle disease virus genome.";
Virology 145:203-212(1985).
- FUNCTION: MOST ABUNDANT PROTEIN IN THE VIRION AND AN IMPORTANT
- FUNCTION:
                                                                                                                                                                                                                 "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB 1; Length 57;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Newcastle disease virus (strain Beaudette C/45) (NDV)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Complete protecome.
SEQUENCE 57 AA; 6688 MW; 7C4A662578176B22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-MAR-1992 (Rel. 21, Last annotation update)
Nucleocapsid protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
              STRAIN=VC-16 / DSM 4304 / ATCC 49558;
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE001028; AAB90166.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.18;
                                                                                                                                                                                                                                                Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; AF1081; -.
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                                                                                                                                                                                                    Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCAP NDVB
P09459;
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NCAP NDVB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PERCISES. typhi; STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougnan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davise R.M., Dowd L., White N., Farrar J., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=S.typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720,
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17; DB 1; Length 57; Pred. No. 2.7e+02;
                                                                  Length 42;
                                                                                                                                    5; Indels
58946F273B21DBB0 CRC64;
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                                                                  Score 17; DB 1;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    57 AA.
                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 413:848-852(2001).
-1- SIMILARITY: BELONGS TO THE GNS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE008780; AAL20724.1; -. EMBL; AL627272; CAD05492.1; -.
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                                                                     54.8%;
                                                                                                    40.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella typhimurium, and
Salmonella typhi.
                               Query Match
Best Local Similarity 40.00,
Laga 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gns protein.
GNS OR STM1809 OR STY1938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 413:852-856(2001).
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RESULT 9
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Best Local (
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P05854;
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                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=85228248; PubMed=2988795;

MEDLINE=85228248; PubMed=2988795;

Crowl R., Ganguly K., Gordon M., Conroy R., Schaber

Shaw G.M., Wong-Staal F., Reddy E.P.;

"HTLV-III env gene products synthesized in E. coli

antibodies present in the sera of AIDS patients.";
an oncogene product.";
Nature 330:266-269(1987).
                        Montagnier L., Lecocq J.-P.;
"HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
                                                                    MEDLINE=88039140; PubMed=3118220; Guy B., Kieny M.-P., Riviere Y.,
                                                                                                                                                                                                                                                                                             NCBI
                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type Viruses; Retrovir
                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1988 (Rel. 09, Creat
01-NOV-1988 (Rel. 09, Last
15-JUN-2002 (Rel. 41, Last
Negative factor (F-protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
SEQUENCE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X14855; CAA32971.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (Rel. 16, Last ar Hypothetical 6.9 kDa protein.
                                                                                                        POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neumann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses;
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                                                                                                                                                41:979-986(1985)
                                                                                                                                                                                                                                                                                           _TaxID=11707;
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57 AA
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Last annotation update)
otein) (27 kDa protein)
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                                                                                                                                                                                                                                                                                                           rus type 1 (HXB3 isolate)
Retroviridae; Lentivirus
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Pred. No.
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                                                                      le Peuch C., Dott
                                                                                                                                                                                                                                                                                                                              (HXB3 isolate) (HIV-1)
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                                                                                                                                                                                                                                                                                                                                                                    (3'ORF) (Fragment).
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RESULT 10
Y049_BORBU
Query Match
Best Local Similarity
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Matches
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051078;
30-MAY-2000
30-MAY-2000
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98065943; PubMed=9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Yugt R., Palmer N., Adams M.D., Goorghey J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artlach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by arentities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                              Hypothetical | SEQUENCE 39
                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00469; F-protein; 1.
ProDom; PD000031; HIV Nef; 1.
AIDS; Myristate; GTP-binding.
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                                                                                                       TIGR; BB0049;
                                                                                                                        EMBL; AE001118; AAC66440.1;
                                                                                                                                                                                                                                                                                                                               Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                           Garland S., Fujii C., Co
Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=ATCC 35210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical BB0049.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=139;
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activities. It seems to down-regulate the CD4(T4) antigen.
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                                                            protein; Complete
AA; 4343 MW; 41
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irochaetales; Spirochaetaceae; Borrelia.
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Pred. No.
  Score 16;
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                     DB 1;
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                   Length 39
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D.,
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(See http://www.isb-sib.ch/announce/
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MEDLINE=94170795; PubMed=8125104;

MARTHIN-Ponthieu A., Wouters-Tyrou D., Pudlo B., Buisine E.,

Martin-Ponthieu A., Wouters-Tyrou D., Pudlo B., Buisine E.,

Isolation and characterization of a small putative zinc finger

protein from cuttlefish epididymal sperm cells.";

Isolation and characterization: Nuclear.

-1 - Subcibulation: Subcaracterization: Subcara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Squalus acanthias (Spiny dogfish).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes;
Elasmobranchii, Squalea, Squaloidei, Squalidae, Squalus.
NCBI_TaxID=7797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01.JUN-1994 (Rel. 29, Created)
01.JUN-1994 (Rel. 29, Last sequence update)
01.JUN-1994 (Rel. 29, Last annotation update)
Epididymal sperm protein E.
Sepia officinalis (Common cuttlefish).
Sepia officinalis (Common Cuttlefish).
Sepia officinalis (Common Cuttlefish).
Sepia officinalis (Common Cuttlefish).
                        and
                                                                                                                                                                                                                                                                                                                                                                                                                            51.6%; Score 16; DB 1; Length 51; ilarity 60.0%; Pred. No. 4.5e+02; Conservative 1; Mismatches 1; Indels
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                        Usage by
                                                                                                                                                                                                                 PERM; PR0471; Ribosomal L13; 1.
ProDom; PD002595; Ribosomal L13; 1.
TIGREAMs; TIGR01023; rpmG bact; 1.
PR051TE; PS00582; RIBOSOWAL L13; 1.
SHibosomal protein; Complete proteome.
SEQUENCE 51 AA; 6045 MW; F45383FA9AB9018B CRC64;
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51 AA; 5967 MW; 0C06D9884EEF6FB8 CRC64;
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01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                  modified and this statement is not removed. entities requires a license agreement (See ) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 AA
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                                                                                                                EMBL; AE004944; AAG08700.1; -. InterPro; IPR002453; Beta tubulin. InterPro; IPR001705; Ribosomal L33.
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les 3; Conserv
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P80304;
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RELX SQUAC
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STRAIN=ATCC 15692 / PAO1;
STRAIN=2043737; Pubmed=10984043;
Stover C. K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
Nature 406:959-964(12000).
-- SIMILARITY: BELONGS TO THE L33P FAMILY OF RIBOSOMAL PROTEINS.
                     Gaps
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-!- SUBCELLULAR LOCATION: Cytoplasmic.
InterPro; IPR006669; Mannitol_dh.
Pfam; PF01232; Mannitol_dh; 1.
Oxidoreductase; NADP.
NON TER 50 50
SEQÜENCE 50 AA; 5648 MW; BEE7F5B6413497FD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gluconobacter oxydans (Gluconobacter suboxydans).
Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
Gluconobacter.
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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Pred. No. 4.4e+02;
1; Mismatches 1; Indels
                     Indels
                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-CCT-2001 (Rel. 40, Last annocation update)
Polyol:NADP oxidoreductase (EC 1.1.1.-) (Fragment).
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15-UTN-2002 (Rel. 41, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
15-UTN-2002 (Rel. 41, Last annotation update)
RPMG OR PAS315.
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Best Local Similarity 60.0
Matches 3; Conservative
                  3; Conservative
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STRAIN=DSM 350;
Klasen R.;
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Best Local 8
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                                                                                                                                                                                                           Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Bill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J. Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
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SEQUENCE.
TISSUE=Ovary;
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PIR; B26463; B26463.
HSSP; P04090; 6RLX.
use by non-profit institutions as long modified and this statement is not removed.
                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                            Nature 406:477-483(2000).
                                                                                                                                                                         cholerae.";
                                                                                                                                                                                                                                                                                                                                              STRAIN=El Tor N16961 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vibrio cholerae
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PROSITE; PS00262; INSULIN; 1.
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Eur. J. Biochem. 161:335-341(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Callard I.P.;
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                                                                                                                                                                                              "DNA sequence of both
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                  European Bioinformatics Institute. The by non-profit institutions as long
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SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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60.0%;
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Pred. No. 4.8e+02;
1; Mismatches 1
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                                                                                                        InterPro; IPR001705; Ribosomal L33. pfam; PF00471; Ribosomal L33; 1. ProDom; PB002595; Ribosomal L33; 1. TIGRPAMs; TIGR01023; rpmG_bact; 1. TIGRPAMs; TIGR01023; rpmG_bact; 1. PROSITE; PS00582; RIBOSOMAL L33; FALSE NEG. Ribosomal protein; Complete proteome. SEQUENCE 55 AA; 6394 MW; 9D7BB702D66367
                                                                                                                                                                                                      EMBL; AE004112; AAF93395.1; TIGR; VC0219; -.
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or send an email to license@isb-sib.ch).
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6394 MW; 9D7BB702D663678A CRC64;
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Pred. No. 4
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Search completed: December 19, 2002, 16:19:43 Job time: 5.55882 secs

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09123 grabidopsis
091242 staphylococ
09241 lactococcus
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042150 ambystoma m
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WEDLINE=20365717; PubMed=10910347;
WEDLINE=20365717; PubMed=10910347;
MEDLINE=20365717; PubMed=10910347;
MEDLINE=20365717; PubMed=10910347;
A Alvarenga R.J. G. Reinach F.C., Arraya J.E., Baia G.S., Baptista C.S., A Alvarenga R.M.C., Carrayo D.M., Carrarer H., A Bueno M.R.P., Camargo A.A., Camargo A.B., Corrayo D.M., Carrarer H., Colutto N.B., Colombo C., Costa R.F., Costa M.C.R., Costa M.C.R., Colutto N.B., Colombo C., Costa P.F., Costa M.C.R., Ferrarer H., A Facincani A.P., Ferrarer A.J.S., Ferraira V.C.A., Ferraro J.A., Ferraro J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., A Farger J.E., Kuramae B.E., Laigret F., Lambais M.R., Leite L.C.C., Lemos B.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Marino C.L., Mardeira A.M.B.N., Madeira M.B.N., Matchino C.L., Mardeira A.M.B.N., Matchino C.L., Mardeira A.M.B.N., Matchino C.L., Mardeira A.M.B.N., Matchino C.L., Mardeira M.C., Coliveira M.A., Nascimento A.L.T.C., Netto L.E.S., Nanno D.H., Nobrega F.G., Nunes L.R., Oliveira M.A., A Monto B.R., Pereira G.A.G., Pereira H.A., Jr., Pereira G.A.G., Referira H.A., Jr., Pereira G.A.G., Roberto B.R., Pereira G.A.G., Santelli R.V., Sawassaki H.E., A de Silva A.C.R., de Silva A.G.R., Callya R.R., Silva W.A. Jr., Roberto P.G., Santellii R.V., Sawassaki H.E., Dr., Jr., de Silva A.G.R., de Silva K.G.R., Saitelli R.R., Silva W.A. Jr., R.
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                          GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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EMBL; AE003951; AAF83980.1; -.

EMBL; AE003951; AAF83980.1; -.

InterPro; IPR000517; Ribosomal L30.

Pfam; PF00327; Ribosomal L30; T.

TIGRPANS; TIGR01308; rpmD_bact; 1.
         STRAIN-LBM192;
STRAIN-LBM192;
Phalen D.N., Wilson V.G., Gaskin J.M., De
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                                                                                                                                  Large T and small t antigens (Fragment).
Budgerigar fledgling disease virus (BFDV).
Viruses; dsDNA viruses, no RNA stage; PolyNCBI TaxID=10625;
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Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
"Genetic Diversity in 20 Variants of the Avian Polyomavirus.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF054402; AAC33626.1; -
InterPro; IPR001623; DnaJ_N.
Pfam; PF00225; DnaJ_1.
SMART; SM00271; DnaJ; 1.
SMART; SM00271; DNAJ_2; 1.
PROSITE; PS50076; DNAJ_2; 1.
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askin J.M., Derr J.N., Graham D.L.; riants of the Avian Polyomavirus."; EMBL/GenBank/DDBJ databases.
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01-NOV-1998 (TrEMBI
01-JUN-2001 (TrEMBI
Large T and small t
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence)
Large T and small t antigens (Fragment).
Budgerigar fledgling disease virus (BFDV).
Viruses; dsDNA viruses, no RNA stage; Polyomaviri
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phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
"Genetic Diversity in 20 Variants of the Avian Polyomavirus.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF054404; AAC33628.1; -.
                                                                Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.; "Genetic Diversity in 20 traiants of the Avian Polyomavirus."; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF054405; AAC33629.1; -.
InterPro; IPR001623; DnaJ N.
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Budgerigar fledgling disease virus (BFDV).
Viruses; dsDNA viruses, no RNA stage; Poly
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       PROSITE;
                               Pfam; PF00226; DnaJ; 1.
SMART; SM00271; DnaJ; 1
                                                                                                                                                                                             STRAIN-ECTX91
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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SMART; SM00271; DnaJ; 1.
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SM00271; DnaJ; 1.
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PS50076; DNAJ_2;
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(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 17, Last annotation updat
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Pred. No. 1.4e
2; Mismatches
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Pred. No. 1.4e+02;
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01-NOV-1998 (TrEMBLrel. 08, Created)
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Large T and small t antigens (Fragment).
Large T and small t antigens (Fragment).
Viruses; dsDNA viruses, no RNA stage; Polyomavirus.
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Budgerigar fledgling disease virus (BFDV).

Viruses, dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.

NCBI_TAXID=10625;
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Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
"Genetic Diversity in 20 Variants of the Avian Polyomavirus.";
Submitted (MAR-1998) to the BMEL/GenBank/DDBJ databases.
EMBL; AF054408; AAC33632.1;
InterPro; IPR001623; DnaJ.N.
Pfam; PF00226; DnaJ; 1.
SWART; SW00271; DnaJ; 1.
PROSITE; PS50076; DNAJ_2; 1.
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Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
"Genetic Diversity in 20 Variants of the Avian Polyomavirus.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, APOS4409; AAO33633.1;
InterPro: IPR001623; DnaJ.N.
PROM: PP00226; DnaJ; 1.
SWART; SM00271; DnaJ; 1.
PROSITE; PS50076; DNAJ_2; 1.
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Pred. No. 1.4e+02;
2; Mismatches 3; Indels
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Pred. No. 1.4e+02;
2; Mismatches 3; Indels
          Indels
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(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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54.5%;
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23 KTAYRRTALKY 33
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23 KTAYRRTALKY 33
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23 KTAYRTALKY 33
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01-JUN-2001
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 17, Last annotation update)
Large T and small t antigens (Fragment).
Budgerigar fledgling disease virus (BFDV).
Viruses; denny viruses, no RNA stage; Polyomavirus.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Large T and small t antigens (Fragment).
Budgerigar fledgling disease virus (BFDV).
Viruses; dsDNA viruses, no RNA stage; Polyomavirus.
NCBL_TAXID=10625;
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STRAIN=LB85;
STRAIN=LB85;
Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
INTER-AFO54406; AAC33630.1;
InterPro; IPRO1623; DnaJ_N.
Pfam; PF00226; DnaJ; 1.
PROSITE; PS50076; DNAJ; 1.
PROSITE; PS50076; DNAJ, 2; 1.
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                                                                         Score 30; DB 12; Length 54; Pred. No. 1.4e+02; 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30; DB 12; Length 54;
Pred. No. 1.4e+02;
2; Mismatches 3; Indels
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                            5AF094925DE8C997 CRC64;
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PROSITE; PS50076; DNAJ_2; 1.
     54
6077 MW;
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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23 KTAYRRTALKY 33
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23 KTAYRRTALKY 33
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Best Local :
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Ol-NOV-1998 (TrEMBLrel. 08, Last sequence update)
Ol-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Large T and small t antigens (Fragment)
Budgerigar fledgling disease virus (BPDV)
Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
NCBI TaxID=10625;
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"Genetic Diversity in 20 Variants of the Avian Polyomavirus.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF054411; AAC336351; --
InterPro; IPR001623; DnaJ_N.
Pfam; PF00226; DnaJ; 1.
SMART; SM00271; DnaJ; 1.
SMART; SM00271; DNAJ; 1.
PROSITE; PS50076; DNAJ_2; 1.
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SEQUENCE
089899
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Pfam; PF00226; DnaJ; 1.
SMART; SM00271; DnaJ; 1.
PROSITE; PS50076; DNAJ_2; 1.
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EMBL; AF054412; AAC33636.1; -.
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Budgerigar fledgling disease virus (BFDV)
Viruses; dsDNA viruses, no RNA stage; Pol
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Pred. No.
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RESULT 14
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  089901;
01-NOV-1998
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Large T and
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01-NOV-1998
01-JUN-2001
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STRAIN-EDGRABI-B;
Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
"Genetic Diversity in 20 Variants of the Avian Polyomavirus.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF054413; AAAC33637.1;
InterPro; IPR001623; DnaJ_N.
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Budgerigar fledgling disease virus (BFDV).
Viruses; dsDNA viruses, no RNA stage; Polyomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.; "Genetic Diversity in 20 Variants of the Avian Polyomavirus."; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF054414; AAC33638.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Large T and small t antigens (Fragment).
Budgerigar fledgling disease virus (BFDV).
Viruses; dsDNA viruses, no RNA stage; Poly
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                   (TrEMBLrel. 08, (TrEMBLrel. 08, (TrEMBLrel. 17,
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(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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54.5%;
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Last sequence update)
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s (Fragment)
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Pred. No. 1.4e+02;
2; Mismatches 3
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089902;
01-NOV-1998 (TEMBLrel. 08, Created)
01-NOV-1998 (TEMBLrel. 10, Last sequence update)
01-NOV-2001 (TEMBLrel. 17, Last annotation update)
Large T and small t antigens (Fragment).
Budgerigar fledgling disease virus (BFDV).
Niruses; dsDNA viruses, no RNA stage; Polyomavirus.
NIBI_TAXID=10625;
Budgerigar fledgling disease virus (BFDV).
Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
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P. SEQUENCE FROM N.A.

RA Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;

RA STAIN-LIBEL93;

RA Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;

RI Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

BR EMBL; AFG04416; AAG33640.1; -.

DR InterPro; IPR001623; DnaJ.N.

DR Ffam; PF00226; DnaJ; 1.

DR SMART; SM00271; DnaJ; 1.

DR PROSITE; PS50076; DNAJ_2; 1.

DR PROSITE; PS50076; DNAJ_2; 1.
                                                                                                                                                                   STRAIN=ECF191;
Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
"Genetic Diversity in 20 Variants of the Avian Polyomavirus.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF054415; AAC33639.1;
InterPro; IRR001623; DnaJ.N.
Pfam; PF00226; DnaJ. 1.
SMART; SM00271; DnaJ; 1.
PROSITE; PS50076; DNAJ. 2; 1.
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Pred. No. 1.4e+02;
2; Mismatches 3; Indels
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Best Local Similarity 54.5
Matches 6; Conservative
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23 KTAYRRTALKY 33
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Search completed: December 19, 2002, 16:21:50 Job time : 22.1765 secs

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Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                         112892 seqs, 41476328 residues
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RET5_BOACN
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Gapop 10.0 , Gapext 0.5
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58
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Nucleic Acids Res. 24:4420-4449(1996).
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Dandekar T., Huynen M., Regula J.T., Ueberle B., Zimmermann C.U.,
Andrade M.A., Doerke T., Sanchez-Pulido L., Snel B., Suyama M.,
Yuan Y.P., Herrmann R., Bork P.;
"Re-annotating the Mycoplasma pneumoniae genome sequence: adding
value, function and reading frames.";
Nucleic Acids Res. 28:3278-3288(2000).
-!- SIMILARITY: BELONGS TO THE S21P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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 Q47270
Q83262
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EMBL; AE000053; AAG34754.1; -.

InterPro; IPR001911; Ribosomal S21.

PROSTIE; PS01181; RIBOSOMAL_S21; FALSE_NEG.

Ribosomal protein; Complete proteome.

SEQUENCE 60 AA; 7515 MW; 30D87DCF4635F003 CRC64;
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Pred. No. 40;
2; Mismatches
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                     REALAS TRREPA
HSP3 HORSE
HSP1 CABFU
HPTA_RABIT
HSS VIBER
PRT3_ONCMY
DRF2_MSSAU
DBF2_MSSAU
DBF2_MSCX_METCL
DBF4_MICSPU
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STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
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16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
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NCBI_TaxID=1582;
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30-MAY-2000
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P19663;
                     MEDLINE=21173623; PubMed=11274389; Folli C., Calderone V., Ottonello S., Bolchi A., Stoppini M., Berni R.; "Identification, retinoid binding and X-ray analyse retinol-binding protein."; Proc. Natl. Acad. Sci. U.S.A. 98:3710-3715(2001).
i- FUNCTION: Intracellular transport of retinol.
                                                                                                                                                                                  TISSUE=Kidney;
                                                                                                                                                                                                                                               NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                         Bovidae; Bovinae;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
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16-OCT-2001
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NON_TER 23 23
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InterPro; IPR000053; Thymid_phosphls.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphorylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Avraham Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=ATCC 7469;
MEDLINE=90381286; PubMed=2119230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
Thymidine phosphorylase (EC 2.4.2.4)
                                                                                                                                                                                                       SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                  Retinol-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Purification and characterization of uridine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactobacillus casei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chim. Biophys. Acta 1040:287-293(1990).

FUNCTION: THE ENZYMES WHICH CATALYZE THE REVERSIBLE PHOSPHORYLOSIS OF PYRIMIDINE NUCLEOSIDES ARE INVOLVED IN THE DEGRADATION OF THESE COMPOUNDS AND IN THEIR UTILIZATION AS CARBON AND ENERGY SOURCES, OR IN THE RESCUE OF PYRIMIDINE BASES FOR NUCLEOTIDE SYNTHESIS.

OR IN THE RESCUE OF PYRIMIDINE BASES FOR NUCLEOTIDE SYNTHESIS.

ORTALYTIC ACTIVITY: Thymidine + phosphate = thymine + 2-deoxy-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE THYMIDINE/PYRIMIDINE-NUCLEOSIDE PHOSPHORYLASES FAMILY. , S11384; S11384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ribose 1-phosphate.
SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLAFRRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLAIRRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
6; Conserv
                                                                                                                                                                                                       AND FUNCTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23
                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 40,
(Rel. 40,
(Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grossowicz N., Yashphe J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from Lactobacillus casei.";
hys. Acta 1040:287-293(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                         Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THYMID_PHOSPHORYLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2752 MW;
                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.6%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation updat
in III, cellular (CRBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8705C9C4D82C1AD7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.
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(TDRPASE)
                                                                                                                                                                                                                                                                                                                                                                                    update)
(CRBP-III)
                                                                                      X-ray analysis
(By similarity)
                                                                                                                                     Bolchi A., Zanotti G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                    (Fragment)
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RESULT 4
H4Y_BLEJA
ID H4Y_BLEJA
AC P80738;
DT 01-NOV-1997
                                                                                                                                                                                       RESULT 5
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Best Local S
Matches 6
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Matches
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                                                            01-AUG-1992 (Rel. 2
01-AUG-1992 (Rel. 2
01-NOV-1997 (Rel. 3
Small hydrophobic p
                                                                                 VSH MUMPB
P28082;
01-AUG-1992
01-AUG-1992
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; |
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chromosomal protein; Nucleosome NON_TER 47 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cillophora, Heterotrichida).",
FEMS Microbiol. Lett. 149:93-98 (1997)
-!- FUNCTION: HISTONE 44, ALONG WITH
IN NUCLEOSOME FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
15-JUL-1999 (Rel.
Viruses; ssRNA negative-strand
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBUNIT: THE NUCLEOSOME IS AN OCTAMER CONTAINING H2A, H2B, H3, AND H4; WHICH WRAP APPROXIMATIVELY -i- SIMILARITY: BELONGS TO THE HISTONE H4 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salvini M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97257506; PubMed=9103980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=A5-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blepharisma japonicum
Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Histone H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vitamin A; Retinol-binding; NON_TER 42 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00061; lipocalin; 1.
PROSITE; PS00214; FABP; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P82980; 1GGL.
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-!- SIMILARITY: BELONGS TO THE
TRANSPORTERS.
                       Mumps virus (strain Belfast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salvini M., Bini E., Santucci A., Batistoni R.; "H4 histone in the macronucleus of Blepharisma japonicum (Protozoa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=5961;
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                                                                                                                                                                                                                                                                         36
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                                                                                                                                                                                                                                                                                                                                                      Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PD001827; Histone_H4; 1.
; PS00047; HISTONE_H4; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001951; Histone_H4.
                                                                                                                                                                                                                                                                                                                                                                                                                                      47 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 AA; 4892 MW;
                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                             11
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                                                                                                                                                                      STANDARD;
                                                                               23, Created)
23, Last sequ
35, Last anno
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35, Last
38, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                        4961 MW;
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; Lipocln_cyt
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75.0%;
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:In_cytFABP.
                                                                               sequence update)
annotation update)
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                                                                                                                                                                                                                                                                                                                                                      Score 27; DB
Pred. No. 49;
1; Mismatches

 Mismatches

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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                           D743BEA73B76BADA
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                                                                                                                                                                      PRT;
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viruses; Mononegavirales;
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                                                                                                                                                                      57
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                                                                                                                                                                                                                                                                                                                                                                                               Length 47;
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DB 1; Length 57;
                                                                  61;
                                    Score 27;
Pred. No. 6
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                                                                                                                                                                                                                                                                                                                                                   VSH MUMPM STANDARD; PR. P22112; Ol-AuG-1991 (Rel. 19, Created) 01-AuG-1991 (Rel. 19, Last seque: 01-AuG-1991 (Rel. 19, Last annot Small hydrophobic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                       46.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 AA; 6621 MW;
                                                                                                5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; JU0304; SHNZMS.
InterPro; IPR001477; SH.
Pfam; PF01445; SH; 1.
ProDom; PD001504; SH; 1.
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                                    Query Match
Best Local Similarity
Matches 5; Conserv
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34 YKTAVRHAAL 43
                                                                                                                                                      1 YRLAIRRIAL 10
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34 YKTAVRHAAL 43
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051309;
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                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
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                                                                                    SEQUENCE FROM N.A.
MEDLINE=93168036; PubMed=8435047;
Yeo N.P., Afzal M.A., Forsey T., Rima B.K.;
"Identification of a new mamps virus lineage by nucleotide sequence analysis of the SH gene of ten different strains.";
Arch. Virol. 128:371-377(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDUENCE FROM N.A.
MEDINE-93186036; PubMed-8435047;
Yeo R.P., Afzal M.A.; Forsey T., Rima B.K.;
Tidentification of a new mumps virus lineage by nucleotide sequence analysis of the SH gene of ten different strains.";
Arch. Virol. 128:371-377(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.6%; Score 27; DB 1; Length 57; 50.0%; Pred. No. 61; 3; Indels tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
NCBI TaxID=11170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B8F2F917B4A8EF3C CRC64;
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Paramyxoviridae, Paramyxovirinae, Rubulavirus.
NCBI_TaxID=11166,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Small hydrophobic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mumps virus (strain Bristol 1).
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57 AA; 6814 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001477; SH. Pfam; PF01445; SH; 1. ProDom; PD001504; SH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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ProDom; PD001504; SH; 1.
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34 YKTAVRHAAL 43
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P28083;
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SEQUENCE
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VSH_MUMPL
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STRAIN=ATCC 35210 / B31;
MEDLINE=80805943; PubMed=9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.;
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
   Gaps
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Pred. No. 61;
2; Mismatches 3; Indels
   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mumps virus (strain Miyahara vaccine).
Viruses, ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
NCBI_TaxID=11171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takeuchi K.;
Submitted (NOV-1990) to the EMBL/GenBank/DDBJ databases.
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Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC794E57A4A0F9E6 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                      Pfam; PF00323; defensins; 1.
SMART; SM00048; DEFSN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IS-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DUN-2002 (Rel. 41, Last annotation update)
Neutrophil defensin 1 (HANP-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P81465;
15-DEC-1998
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SEQUENCE 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 390:580-586(1997)
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                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                          Defensin; Antibiotic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hamster neutrophil defensins."
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"Isolation, antimicrobial activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97045125; PubMed=8890190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001271; Defensin_mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Infect.
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YRLCCRR
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                                                                                                                                                                                                                                                                                                 DEFENSIN; 1.
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                                                                                                                                                                                4014 MW;
                                                                                                                                                                                ; Fungicide.
BY SIMILARITY.
31 BY SIMILARITY.
20 BY SIMILARITY.
30 BY SIMILARITY.
4014 MW; 07D8EDFEDCFC1BDA C
                                                                                                                43.1%;
71.4%;
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44 MW; AC
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Pred. No.
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1; Mismatches
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Pred. No.
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ACEC7E55B5A8E0DA
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PSBY_GUITH
RRITAR RRA
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Best Local
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01-OCT-1993
01-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Douglas S.E., Penny S.L.;
"The plastid genome of the cryptophyte alga, Guillardia complete sequence and conserved synteny groups confirm ancestry with red algae.";
J. Mol. Evol. 48:236-244(1999).
-I- FUNCTION: MANGANESE-BINDIAG POLYPEPTIDE WITH L-ARGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSBY_GUITH
078433;
                    Sanson B., Uzan M.;
"Sequence and characterization of the bacteriophage T4 gene product, a possible transcription antitermination J. Bacteriol. 174:6539-6547(1992).
                                                                  SEQUENCE FROM N.A. MEDLINE=93015705;
                                                                                                                             Bacteriophage T4.
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GUITH
                                                                                                     T4-like viruses.
NCBI_TaxID=10665;
                                                                                                                                                       Y00D OR 39.2 OR COMCA.-1.
                                                                                                                                                                  Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      Photosystem
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF041468; AAC35618.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
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MEDLINE=99128221; PubMed=9929392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chloroplast
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15-JUL-1999
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SEQUENCE
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    -i- SIMILARITY: BELONGS TO THE PSBY FAMILY.

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FROM N.A.
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3 (Rel. 27, Last sec
2 (Rel. 41, Last and
al 5.1 kDa protein i
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(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Chloroplast;
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37, Last sequ
38, Last anno
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27, Last sequence up
41, Last annotation
                                                                    PubMed=1400206;
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85.7%;
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                                                                                                                              RNA stage;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                          update)
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                                                                                                                               Caudovirales; Myoviridae;
                                                                                                                                                                            update)
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(See http://www.isb-sib.
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ps confirm its com
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                                   comC alpha
factor.";
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SEQUENCE FROM N.A.
MEDLINE=20123244; PubMed=10659848;
                                                01-NOV-1997 (Rel. 35, Created)
U-NOV-1997 (Rel. 35, Last sequenc
01-NOV-1997 (Rel. 35, Last annotat
Hypothetical 5.5 kDa protein Y4ZD.
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=97305956; PubMed=9163424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000109; AAB91962.1; -.
                                                                                                                                  (strain NGR234).
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Query Match
Best Local Similarity 71.4%,
Sinconservative
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5 IQRISLR 11
                                                                                                                              Rhizobium sp.
                  RHISN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P35310;
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 RESULT 14
HSP1_PONPY
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                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G., Mesyanzhinov V., Ruger W., Stidham T., Thomas E.; "Bacteriophage T4 genome analysis."; Submitted (UUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                           43.1%; Score 25; DB 1; Length 45; 44.4%; Pred. No. 1.2e+02; tive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.1%; Score 25; DB 1; Length 57; 50.0%; Pred. No. 1.6e+02; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mumps virus (strain Takahashi).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (NOV-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                             45 AA; 5107 MW; 4E550618271A1257 CRC64;
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01-AUG-1991 (Rel. 19, Last sequence update)
01-AUG-1991 (Rel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 AA.
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                                                                                                                                                                                                          EMBL; M89919; AAA32486.1; -.
EMBL; AF158101; AAD42464.1; -.
PIR; D45731; D45731.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D90235; BAA14283.1; -.
PIR; JU0309; SHNZMT.
InterPro; IPR001477; SH.
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57 AA; 6745 MW;
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Small hydrophobic protein.
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Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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ProDom; PD001504; SH; 1.
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tes 5; Conserv
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34 YKTAMRHAAL 43
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P22113;
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Matches
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VSH_MUMPT
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RESULT 13

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"Rapid evolution of male reproductive genes in the descent of man.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 403:304-309(2000).
-!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
                                                                                                                                                                                                                                                                                                                                                                                                                                   Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
MCBI_TaxID=9600;
                                                                                                                                                                   Plasmid sym pNGR234a.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.
NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 387:394-401(1997).
-!- SIMILARITY: NONE OBVIOUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Retief J.D., Winkfein R.J., Dixon G.H., Adroer R., Queralț
Ballabrigo J., Oliva R.;
"Evolution of protamine P1 genes in primates.";
J. Mol. Evol. 37:426-434(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.4%; Score 24; DB 1; Length 49; 71.4%; Pred. No. 2.1e+02;
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SEQUENCE 49 AA; 5514 MW; 6BICF7141547BD0D CRC64;
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01-FEB-1994 (Rel. 28, Last sequence update)
01-UJN-2002 (Rel. 41, Last annotation update)
Sperm protamine P1 (Cysteine-rich protamine).
Last sequence update)
Last annotation update)
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P22111;
01-AUG-1991
                                                                                                                                                                                   TRANSMEM SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content to the modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
                                                                                                                                                                                                                                                                                            Pfam; PF01445; SH;
                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (NOV-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mumps virus (strain Matsuyama).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-AUG-1991 (Rel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L14589; AAA36946.1; -. EMBL; AF215710; AAF34623.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                 ProDom; PD001504; SH; 1.
                                                                                                                                                                                                                                                                                                                                                                   EMBL; D90233; BAA14281.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=11165;
                                                                                                                                                                                                                                      Fransmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000221; Protamine_P1.
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1 YRLAIRRIAL 10
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SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: TESTIS.
SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                JU0307; SHNZMM.
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                                                                                                                                                                                                                                                                                                                        IPR001477; SH.
                                                                                                                                                                                     57 AA;
                                                                                 Conservative
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6697 MW;
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                                                                                                         Score 24; DB 1; Length 57; Pred. No. 2.5e+02;
                                                                                                                                                                                     POTENTIAL.
1D994E57AA55ECF0 CRC64;
                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57
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Db 34 YKTAVRHASL 43

Search completed: December 19, 2002, 16:19:42 Job time: 5.47059 secs

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version 5.1.3
- 2002 Compugen Ltd.
  GenCore
Copyright (c) 1993
```

OM protein - protein search, using sw model

December 19, 2002, 16:16:02; Search time 10.4118 Seconds (without alignments) 110:799 Million cell updates/sec Run on:

US-08-653-294C-36 58 1 YRLAIRRIALRY 12 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

15911

Minimum DB seq length: 0 Maximum DB seq length: 60

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* 2 E 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

SH	Description	508 ribosomal prot	hypothetical prote		О	glyceraldehyde-3-p	small hydrophobic	small hydrophobic	hypothetical prote	hypothetical prote	, hypothetical prote	Ig heavy chain DJ	hypothetical prote	a]	gene 39.2 protein	hypothetical prote	small hydrophobic	small hydrophobic	hypothetical prote	hypothetical prote		hypothetical prote	C	probable RNA [impo	hypothetical prote		prostaglandin E2 r	hypothetical prote		
SUMMARIES		4	0	7	4	2	ξĊ	Съ	H	2	0	2	80	7	7	9	Ħ	80	6	0	80	σ	Ŋ	9	7	Ŋ	5	9	۳	4
OS:	ID	C82714	D84640	A86702	S11384	A60475	SHINZMS	SHNZBE	B70141	AF2002	E82080	PH1335	A82288	AB0747	D45731	T31016	SHNZMI	JQ2368	AB1589	AI1650	T12018	AE1889	CS5995	G90716	G64801	S29785	D55995	C84186	82	D8257
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	Length	53	52	28	24	34	57	57	51	52	55	28	33	38	45	52	57	57	28	58	59	59	39	39	39	44	48	52	53	54
di	Query	51.7	48.3	48.3	46.6	46.6	46.6	46.6	44.8	44.8	44.8	43.1	43.1	43.1	43.1	43.1	43.1	43.1	43.1	43.1	43.1	43.1	41.4	41.4	41.4	41.4	41.4	41.4	41.4	41.4
	Score	30	28	28	27	27	27	27	26		26	25	25	25	25	25	25	25	25	25	25	25	24		24	24	24	24	24	24
	Result No.		7	Ю	4	S	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

small hydrophobic ribonucleoside-dip small hydrophobic	phosphofructokinas ycf32 protein - Od ribosomal protein hynorherical profe	hypothetical prote ribosomal protein 508 ribosomal prot ribosomal protein	hypothetical prote hypothetical prote hypothetical prote hypothetical prote small hydrophobic
SHNZMM C41476 S24827	JC4218 S78239 T07519	A81550 JC1154 E84931 C64388	S58608 F70209 B69161 G98149 SHNZMU
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57	33 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4444	55 53 53 54 54 54 54 54 54 54 54 54 54 54 54 54
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0 0 0 4 4 4	7 2 2 2 2	23333	23333
30 31	. W W W W	3333 388 409	4 4 4 4 1 2 2 4 2

## ALIGNMENTS

RESULT

C82714 50S ribosomal protein L30 XF1170 [imported] - Xylella fastidiosa (strain 9a5 C;Species: Xylella fastidiosa
<pre>C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000 C;Accession: C82714</pre>
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucle Nature 406, 151-157, 2000
A, Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;xererence number: A82515; Muln:20355/1/; FMID:1091034/ A;Note: for a complete list of authors see reference number A59328 below
A,Accession: C82714 A,Status: preliminary
A;Molecule type: DNA A;Residues: 1-53 <sim></sim>
A; Cross-references: GB: AE003951; GB: AE003849; NID: 99106131; PIDN: AAF83980.1;
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alva
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.W
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to Confirm Time 2000

eotide Sequen

2c)

rarenga, R.; A M.; Carrer, H ; GSPDB:GN001

submitted to GenBank, June 2000

Abuthors: Ferranca, S.C.; Franco, M.C.; Frohn
J.D.; Junqueira, M.L.; Kemper, B.L.; Kitajian, J.P.; Krieger, J.E.; Kuramae, B.E.; Laign
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, P.
A.Puthors: Martins, B.M.F.; Mateukuma, A.Y.; Manck, C.F.N.; Miscaca, E.C.; Miyaki, C.Y.,
F.G.; Nunes, M.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A.Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva,
A.Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: Escherichia coli ribosomal protein L30

٥; h Similarity 45.5%; Pred. No. 63; 5; Conservative 4; Mismatches 2; Indels Best Local Similarity Matches 5; Conserv Query Match

ö

Gaps

1 YRLAIRRIALR 11 :||::| : || 14 HRLSVRALGLR 24 ò a

RESULT 2
D84640
hypothetical protein At2g24780 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001
C;Azes: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001
C;Azes: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

```
thymidine phosphorylase (EC 2.4.2.4) - Lactobacillus W,Alternate names: pyrimidine phosphorylase C;Species: Lactobacillus casei C;Date: 19-Mar-1997 #sequence_revision 26-Feb-1998 #t C;Accession: S11384
                                                                    A;Experimental source: strain ATCC 7469
A;Note: this protein was shown to possess thymidine phosphorylase C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase C;Keywords: glycosyltransferase; homodimer; pentosyltransferase
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A;Accession: A86702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84640
A;Accession: D84640
                                                                                                                                                 A; Molecule type: protein
A; Residues: 1-24 < AVR>
                                                                                                                                                                                                          R;Avraham, Y.; Grossowicz, N.; Yashphe, J. Biochim. Biophys. Acta 1040, 287-293, 1990 A;Title: Purification and characterization A;Reference number: S11383; MUID:90381286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-52 <STO>
                                                                                                                                                                                     A; Accession: S11384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: At2g24780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE002093; NID:g4559373; PIDN:AAD23034.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            euss, D.; Nierman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ypothetical protein ygaF [imported] - Lactococcus lactis subsp. lactis (st
;Species: Lactococcus lactis subsp. lactis
;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
;Accession: A86702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                 46.6%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.3%;
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Pred. No.
                   Score 27; DB 2;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 28; DB 2;
Pred. No. 1.7e+02;
Mismatches
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                                                                                                                                                                                                                                                                                                   26-Feb-1998 #text_change 21-Nov-1998
                                                                                                                                                                                                          of uridine and thymidine phosphorylase from PMID:2119230
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                                     Length 24;
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                                                                                        C;Species: mumps virus
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992
C;Accession: S19866
R;Yeo, R.P.; Afzal, M.A.; Forsey, T.; Rima, B.K.
submitted to the EMBL Data Library, January 1992
A;Description: Nucleotide sequence analysis of the A;Reference number: S19866
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SHNZMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:D90234; NID:g222162; PIDN:BAA14282.1; C;Superfamily: mumps virus small hydrophobic protein C;Keywords: transmembrane protein C;Keywords: transmembrane #status predicted <TM1> F;13-29/Domain: transmembrane #status predicted <TM1>
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                   A;Cross-references: EMBL:X63709; NID:g60596; PIDN:CAA45242.1; PID:g60597
                                     A; Molecule type: DNA
A; Residues: 1-57 < YEO>
                                                                                                                                                                                                                          SHNZBF small hydrophobic protein - mumps virus (strain Belfast)
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A; Residues: 1-57 < TAK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Takeuchi, K.
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C;Keywords: oxidoreductase
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A; Residues: 1-34 <FRO>
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;Date: 31-Mar-1993 #sequence_revision
   Genetics:
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Pred. No. 1.6e+02;
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3;
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Cidatesion: D.; Ermolaeva, M.D.; Vamathevan, W.J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: DNA
A,Residues: 1-55 <HEI>
A,Cross-references: GB:AE004310; GB:AE003852; NID:g9656963; PIDN:AAF95536.1; GSPDB:GN001
A,Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain DJ region (clone C155-137) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1335
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
A;Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lympl A;Reference number: PH1302; MUID:93094761; PMID:1460419
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A,Residues: 1-33 <HEI>
A,Cross-references: GB:AE004159; GB:AE003852; NID:g9655167; PIDN:AAF93900.1; GSPDB:GN001
A,Experimental source: serogroup O1; strain N16961; biotype El Tor
                                    01)
                                    ypothetical protein VC2393 [imported] - Vibrio cholerae (strain N16961 serogroup
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 55;
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50.0%; Pred. No. 3.2e+02;
tive 2; Mismatches 3;
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Best Local Similarity 50.04
Matches 5; Conservative
                                                                    C;Species: Vibrio cholerae
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Best Local Similarity
Matches 5; Conserv
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11 VVIRLLLERY 20
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A; Residues: 1-28 < WAS>
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37 LGIKRVAL 44
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A;Gene: VC2393
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PH1335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
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A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AF2002
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A, Residues: 1-52 «KUR»
A; Residues: 1-52 «KUR»
A; Cross-references: GB: BA000019; PIDN: BAB77938.1; PID:g17135392; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                      Ppothetical protein BB0331 - Lyme disease spirochete
Species: Borrelia burgdorferi (Lyme disease spirochete)
Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
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                                                                                                                 Query Match 46.6%; Score 27; DB 1; Length 57; Best Local Similarity 50.0%; Pred. No. 2.6e+02; Matches 5; Conservative 2; Mismatches 3; Indels
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C;Superfamily: mumps virus small hydrophobic protein C;Keywords: transmembrane protein F;8-29/Domain: transmembrane #status predicted <TVM>
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Best Local Similarity
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Matches 6; Conserv
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34 YKTAVRHAAL 43
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13 LKLRRAILKY 22
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C; Genetics:
A; Gene: VC0735
A; Map position:
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A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
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                                                                                             R;Sanson, B.; Uzan, M.
J. Bacteriol. 174, 6539-6547, 1992
A;Thile: Sequence and characterization of the bacteriophage T4 comCalpha gene product, A;Thile: Sequence and characterization of the bacteriophage T4 comCalpha gene product, A;Reference number: A45731; MUID:93015705; PMID:1400206
                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: host Escherichia coli
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Oct-1999
C;Accession: JS0564; D45731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names:
C;Species: phage T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene 39.2 protein - phage T4
N;Alternate names: gp 39.2
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                       A;Molecule type: DNA
A;Residues: 1-45 <SAN>
                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-37 <HUA>
                                                                                                                                                                                                                                                                                                                                                                           R;Huang, W.M.
Nucleic Acids Res. 14, 7751-7765, 1986
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A; Residues: 1-38 < PAR>
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A;Cross-references: GB:M89919; NID:g215829; PIDN:AAA32486.1; PID:g215833
                                                                        A;Accession: D45731
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                                                                                                                                                                                          A;Cross-references: GB:X06220; NID:g728616
A;Note: this ORF is not annotated in GenBank entry MYT4G39
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                                                                                                                                                                                                                                                                                                Title: Nucleotide sequence of a type II DNA topoisomerase gene. Bacteriophage T4 gene;Reference number: A25763; MUID:87040739; PMID:3022233;Accession: JS0564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: GB:AL513382; PIDN:CAD05677.1; PID:g16503172; GSPDB:GN00176
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R;She, Q.; Phan, H.; Garrett, R.A.; Albers, S.V.; Stedman, K.M.; Zillig, W. Extremophiles 2, 417-425, 1998
A;Title: Genetic profile of pNOB8 from Sulfolobus: the first conjugative plasmid from an A;Reference number: Z20959; MUID:99044580; PMID:9827331
A;Accession: T31016
                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-52 <SHE>
A;Cross-references: EMBL:AJ010405; NID:el351926; PID:el351938; PIDN:CAA09122.1
A;Experimental source: strain NOB8H2
Search completed: December 19, 2002, 16:22:56 Job time: 11.4118 secs
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                                                                                                                                                                                                                  A; Genome: plasmid pNOB8
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44.4%;
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Pred. No. 5.8e
2; Mismatches
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Pred. No. 5e+02;
1; Mismatches
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5.8e+02;
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